CB420818 593806 MB
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BY536666 BY536666
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AA03499 BXA403499
AL411257 T7 end of
AL0371053 Drosophil
BX456575 BX456575
AL274417 Terraodon
AL174271 Terraodon
AL174271 Terraodon
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AC160661 Pan troog
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AL300860 Terraodon
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CNS0145P
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CNS0161D
BX360615
CNS010MP
BX46269
CNS010MP
AL5355654
BX46296
CNS010MP

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AU185777 663 bp mRNA linear EST 05-JUL-2001 AU185777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens CDNA clone B02302-019, mRNA sequence.
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1 (bases 1 to 63)

2 (bases 1 to 63)

2 (bases 1 to 63)

2 (bases 1 to 63)

Contact: Yuji Sugita

Genox Research, Inc.

907 Nogawa, Miyamae-Ku, Kawasaki, Kanagawa 216-0001, Japan

Tel: 81-44-797-2281

Fax: 81-44-797-2281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: syuji@genox.co.jp, URL: http://www.genox.co.jp.
Location/Qualifiers
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AU185777.1 GI:14623690
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     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/mol_type="maxna"
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Sfil (ggccattatggcc); Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned.
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CacGCCCATTATGGCC.3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCACATG-dT(30)BN-3' (where B = A,
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RPCI-23-30A15.TV RPCI-23 Mus musculus genomic clone RPCI-23-30A15,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M. Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCACACAACCATCATTAGAAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTTATTCCAATAACATTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 TTTTGGGATTTTTAATTTTCAAACACAGCAGAATGACATTTTTTTCTGTCACTATTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GITGGIATGIGAGCTATITGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAAATGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can b
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.e column: 19
Plate: NDCM151 row: e column: 19
High quality sequence stop: 488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 268.2; DB 14;
Pred. No. 3e-42;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGACTCCTACCAAAGCTGTCAAAACCACAGG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGACTCCTACCAAAGCTGTCAAAAACAACGG
                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ121459.1 GI:7788387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.6%;
llarity 98.9%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 270; Conserv
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Crarrhini; Hominidae; Homo.

1 (bases 1 to 659)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,M. Tr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deolivaira,P.S., Bucher,P., Jongeneel,C.V.,
Santes,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV721179 HTB Homo sapiens cDNA clone HTBAKF11 5', mRNA sequence.
AV721179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-MT0267-Seq primer: puc 18 forward.

High quality sequence stop: 639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
/clone lib="MT0267"
/note="Corgan: marrow Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwyg Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTATTTGGAGGTCCAATTCAGGAAGCAACACTTGGAGAATGGCTACTTTCTATCAAGA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AATAAAGAGGACACACAGTCAACCCACACATCATCTTTAGAAGACAGTGTGACTCCTACC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 AATAAAGAAACCACAGTCAACCCACACACACATCTTTAGAAGACAGTGTGACTCCTTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 659;
                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.4%; Score 138.4; DB 12; Length 99.3%; Pred. No. 4.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 AAAGCTGTCAAAACCACAGG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGCTGTCAAAACCACAGG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV721179.1 GI:10818331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .659
                                                                                                                                                                                                                                                                                                       sequence tags
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                                                                                                                                                                                                                                                                                                                                                                          .0737800
                                                                                                                                                                                                                                                                                                                                                   20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452
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Best Local S
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ACCESSION
VERSION
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SOURCE
ORGANISM
     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                MEDLINE
PUBMED
COMMENT
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AV721179
LOCUS
                                                                                                     REFERENCE
                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //sex="Female"
/lab host="BH10B"
/clone_lib="RPCI-23"
/note="Crgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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BIO18962
BIO18962.1 GI:14425592
EST.
                                                                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate:30 row: A column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 AACATACAGTTTATTTATCAATAACCATAGGCATCCCCTATATATGTCCCATAAAATATGA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GITTIGGGATITITAATITICAAACACAGCAGAATGACAI--TITITCTGTCACTATTAIT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 GTTCGTGACGTATGAAGCATTTTTGGTGACACAATTCAGGGAGAAATCCAGAGGAGAAAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ATTGTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTACTITICIATCAAGAAATAAAGAGAACCACAGTCAACCCCACACACTCTTTAGAAGA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 CAGTGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGA---- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 CAACTICCTATCAAGAAATAAAGAGAACCACA---AGCCCACAGAATCATCTTTAGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 GGGATCCCGGATTCCAGAGGTTCATTTCCTGGTGCTGAGGCCTGGGGGG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 147.6; DB 28; Length 663; larity 71.6%; Pred. No. 7.3e-19; Conservative 0; Mismatches 89; Indels 11;
                  Other GSSs: RPCI-23-30A15.TJ
Conteact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 938 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:10090"
/clone="RPCI-23-30A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: T7
Class: BAC ends.
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BI018962/c
LOCUS
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us-09-989-293a-376.rst

TITLE JOURNAL COMMENT

FEATURES

ORIGIN

REFERENCE AUTHORS

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SES Okazakly. Puruno, M. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaddo, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Goldbori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Bult, C., Schonbach, G., Schrim, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissic, C., Godzik, A., Grammond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Javvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V. Lee, Y., Lendrad, B., Loyns, P.A., Maglott, D.R., Nantais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Peetrovsky, N., Pillai, R., Pontus, Ju., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.B., Teasdale, R.D., Tomita, Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yun, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Waki, K., Kawai, J., Natawa, K., Arakawa, T., Fukuda, S., Hashizaki, Y., Sasaki, D., Shibata, K., Rapinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, Fansich Parakawa, I., Bhiray, R., Shiraki, R., Sasaki, D., Shibata, R., Rogers, J., Billary, R., Shiraki, R., Sasaki, D., Shibata, R., Rogers, J., Billary, R., Shiraki, R., Shiraki, R., Sasaki, D., Shibata, R., Rogers, J., Billary, R., Shiraki, R., Sasaki, D., Shibata, R., Rogers, J., Billary, R., Shiraki, R., Sasaki, D., Shibata, R., Rogers, J., Billary, R., Shiraki, R., Shiraki, R., Sasaki, D., Shibata, R., Ragis, R., Shiraki, R., Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BYS47544 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730119008 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 GCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 GGTATTTGGAGATCCAGTTCAGGGAACAACCTGTTGAAGAGTGACAGCTTTCCATCAAGA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 AATAAAGAGAACCACAGTCAACCCACAATCATCTTTAGAAGACAGTGTGACTCCTACC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                    /mol type="mmkNa"
/db xref="taxon:9913"
/db xref="taxon:9913"
/lab bost="DH10B"
/clone lib="WARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
lincluding liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                                                                                                                                                                                                                                                             Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                                                                                                                                                                                                                                                                                                                                                             Score 104.8; DB 14
Pred. No. 1.5e-10;
0; Mismatches 22;
      organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AAAGCTGTCAAAACCACAGG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 AAGGCTCTCACGACCACAGG 383
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                                                                                                                                                                                                                                                                                                                                                                                             14.7%;
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Best Local Similarity
Matches 118; Conserva
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BY547544
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KEYWORDS
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FOYBO14 row: B column: 7
Seq primer: GTAATACGACTCACTATAGGG.
                 (bases 1 to 673)

Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,M., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Homo sapiens cDNA HTB clones

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 582)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Fray,J.B. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 25-MAR-2003
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="HTB"
/note="Vector: pBluescript sk(-); Site_1: BcoRI; Site_2:
                                                                                                                                                                                                                                                     Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
Chinese Shoujng Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hars@eApg.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCCACACAATCATCTTTAGAAGACAGTGTGACCTCCTACCAAAGCTGTCAAAACCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 AGGAAGCAACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACACCACAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 ACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTCAAAACCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAAACCACAGTCA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          רטיפינו אתאה 592 bp mRNA linear 593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
CB420918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%; Score 120; DB 9; I 100.0%; Pred. No. 1.6e-13; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="Hypothalamus"
dev_stage="Adult"
lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="mRNA"
|db_xref="taxon:9606"
|clone="HTBAKF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB420818.1 GI:29187264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Bos taurus
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Best Local S:
Matches 120,
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DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 6 CB420818

Op

à g à ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

MEDLINE

source

FEATURES

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Email: genome-res@gsc.riken.go.jp,
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Saaski, D., Sato, K., Shibata, K.,
Shizaki, T. Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational haalysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequence Mamu. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libracties for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse fill-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Davision of Experimental Animal Research in Riken contributed to
                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse issues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Combining Addebrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 GITITIGGGATITITAATITITCAAACACAGCAGAATGACAT--TITITICIGICACIATIAIT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AACATACAGITTATTTATTATCAATAACCATAGGCATCCCCTATATATGTCCCATAAAATATGA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 ATTGTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 GTTCGTGACGTATGAAGCATTTTGGCGACACAATTCAGGGAGAAATCCAGAGAGAAAGA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AATATATCATCTATTTATCATTAATCAATAATGTATTCT-TTTATTCCAATAACATTTGG
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Pred. No. 5e-05;
); Mismatches 54; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="F730119008"
                              Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            we dendritic cells"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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69.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACTICCT
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Sokazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,T., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schrinl,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Eletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T. A.,
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Nuncckin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Majlott,D.R.,
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Mayasai,T., Yang,Z., Zavolan,M., Zhu,Y., Zamer,A., Yanagisawa,M., Yang,I.,
Yang,L., Yan,Z., Zavolan,M., Zhu,Y., Zamer,A., Yanagisawa,M., Yang,I.,
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Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Analyais of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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URL:http://genome.gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Arakawa,T., Itob,M., Kawai,J., Konno,H.,
Hirozane,T., Imotani,K., 18hii,Y., Itob,M., Kawai,J., Konno,H.,
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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length conva libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384 format
        EST 14-DEC-2002
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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BYS36666 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus CDNA clone F630311P20 3', mRNA
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                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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                 prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Adebrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                    /cell_type="NOD-derived CD11c +ve dendritic cells" /clone_lib="RIKEN full-length enriched, NOD-derived CD11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 GTTCGTGACGTATGAAGCATTTTGGCGACACATTCAGGGGAGAAATCCAGAGGAGAAGA 410
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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http://image.llnl.gov
Plate: LLAM1101 row: j column: 08
High quality sequence start: 27
High quality sequence stop: 825.
Location/Qualifiers
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Pred. No. 4.8e-05;
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                                                                                                                                                                                 1. .419
/organism="Mus musculus"
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/clone="F630311P20"
                                                                                                                                                                                                                                                                                                                                              +ve dendritic cells"
                                                                                                                                      further details.
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Submitted (12-JUM-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefagenoscope.cns.fr
- Web: www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGe. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on Dw sp, the same strain used for the BDGP's pi and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillers for physicialzation from the BACFAC Resource Center can be found at http://warnar.mad.wi/Arrosowila har htm.//hacmac mad.wi/Arrosowila har htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR8K10 of RPCI-98 library from Drosophila melanogaster (fruit AL063921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                     /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
| Jab host="Mal0" |
| /lab host="Mal0" |
| /lone lib="NCI_CGAP_Lu29" |
| /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1; |
| Site_2: Not1; Cloned unidirectionally, Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 AGCATTATGGAGACACAATTCAGGGAGAAATCCAGAAGAGAAAAGACAACTTCCCATCAAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 AAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 AAATAAAGAGAAACCACACACACAGAATCATTTTAGATGAGAAGGTGGCTCCCTC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endoptera, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 73.8; DB 12; Length 855; Pred. No. 0.00013; 0; Mismatches 32; Indels 3
                                                                                                                                                                                                                                                                                                                                                  providing samples: Gilbert Smith, NIH
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Drosophila melanogaster
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/db_xref="taxon:7227"
/db_xref="taxon:10090"
/clone="IMAGE:5036647"
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/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 CAAAGCIGICAAAACCACAGG 273
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Best Local Similarity 75.2%;
Matches 106; Conservative (
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/tissue type="PLACENTA"

/close lib="Homo sapiens PLACENTA"

/close lib="Wector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO6QXV 1759 bp DNA linear GSS 05-JUL-2001 T7 end of clone AWOAA009409 of library AWOAA from strain CLIB 89 of Yarrowia lipolytica, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     909
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Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
                                                                                                                                                                                                                                                                                                                                                                        547 ATCTACAGGAGATCATATAATTTGATACAAATAAAAGGAAAAGTGTTCTCTCCCCTTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTGGACTTTATTAAATTTTAAAATCAGTAACTGATTTTATCACTGGCTATGTGCTTTAG
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                                                                                                                                                                                                                                                                                                                    Gaps
 InVitroGen Corporation 1600 ID : CLOBA002ZH05FP1.
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                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                 Score 56; DB 13
Pred. No. 0.46;
http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
Location/Qualifiers
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FEBS Lett. 487 (1), 95-100 (2000)
20584727
                                                                 organism="Homo sapiens"
                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BA002ZH05"
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BX403499 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA002ZH05
3-PRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@llfetech.com URL
                                                                                                                     ||||::::|:|::::|::::|
AATDWWWGWADADWWTWDAWADDRWDAWAWKWDDAWAWGARTADRRDWGGRAGK
                                                                                                                                                                                                                                                                                                                                                                 AAAGCTGTCAAAACCACAGGCAAAGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 ACTITIATIAATITITAAAATCAGIAACTGAITITATCACTGGCTAIGTGCTIAGAICTACA
                                                                                               TITATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGATTTTGGGATTTTTA
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                                  Length 1101;
                                                                Indels
                                DB 29;
                                                              Mismatches 277;
                                Score 58.6; DB Pred. No. 0.11;
                                                                Conservative 251;
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                                8.2%;
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Homo sapiens
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- when you were the main is segretegenoscope.cns.fr

- web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazucyo Gosegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCT-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain v2; on bw sp, the same strain used for the BDGP's

pl and BST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library

and how to order individual BAC clones, the entire library,

and how to order individual from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNSO6FSV 11-JUN-2001 T7 end of clone AROAA032H05 of library AROAA from strain CBS 732 of Zygosaccharomyces rouxii, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTGGCTATGTGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAWITICWAAAAIIMWAAWIWMIAAWIAWAAIIWAITATWAAYWAYAAAAAAAAAAA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589 IGTICICICCCCTTACAGAATIGACAITTTAAATGCGATACAGTTAGAATAGGAAATAIG 648
                                                                                                               - Centre National de Sequencage
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Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 55.6; DB 29; Length 40.3%; Pred. No. 0.42; Live 45; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|db_xref="taxon:7227"
                                                                                            Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BACR31021"
/clone lib="RPCI-98"
/note="end : TET3"
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                                                                                     Submitted (07-52P-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (B-mail: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr. This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii. Zygosaccharomyces rouxii, Saccharomyces servazzii. Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit AL9), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ААТИТАТИТАТИТАТИТТАТИТИТАТИТАТИТАМАТИТАМАТИТАМАТИТАМАТИТАТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAATTTTTAAAATCAGTAACTGATTT
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Yarrowia lipolytica"
/mol_type="genomic DNA"
/strain="CLIB 89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4952"
/clone="AWOAA009H09"
/clone_lib="AWOAA"
/note="end : T7"
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                               (bases 1 to 759)
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Best Local Similarity 40.4:
Matches 148; Conservative
                                                   Genoscope.
Direct Submission
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         PUBMED
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DNA linear GSS 26-JUL-1999 survey sequence T7 end of BAC
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etde du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 TAAATTGGACTTTATTAATTTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTA 545
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                                                                                                                                                                                                                                                                                                                                                 BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 GATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCCCCTTACA
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                                                               426 CCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTC
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN11G11"
                                                                                                                                                                                                                                                                                                     CNS0145P 1043 bp Drosophila melanogaster genome
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                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey sequence. ALIO3735
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'plasmīd="pBeloBAC11"
'note="end : T7"
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122; Conserv
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CNS0145P/c
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolyfica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the other extremity of this sequence and for the sequence of the other extremity of this insert.
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           1 (bases 1 to 895)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigmy,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 IGCAGTIGGCIGGACAGTICTAAATIGGACTITTATTAATITTTAAAAICAGTAACIGAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 TTACCTTAGTGTAATGTATCCCTGTCATATACAATAAGGTGAAATTATAAGTACCCTA
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                                                                                                                                                                                                                                                                                 2 (bases 1 to 895) de Montigny, T., Straub, M., Potier, S., Tekaia, F., Dujon, B., Winoker, P., Artiguenave, F. and Soucier, J. Genomic exploration of the hemiascomycetous yeasts: 8.
  Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces
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/note="putative mitochondrial tRNA_thr gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zygosaccharomyces rouxii"
/mol_type="genomic DNA"
/strain="CBS 732"
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                                                                                                                                                                                                                                                                                                                                                                       Zygosaccharomyces rouxii
FEBS Lett. 487 (1), 52-55 (2000)
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/clone="AR0AA032H05"
/clone_lib="AR0AA"
/note="end : T7"
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                    REFERENCE
AUTHORS
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Search completed: April 4, 2004, 06:03:36 Job time: 2705 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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STIMMARTES

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		Description	Sequence	Sequence													
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		BB	6	δ	σ	Q	σ	9	σ	σ	σ	9	σ	σ	σ	σ	σ
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d	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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-066-60	US-09-991-181-376	-989-730-37	0-436-37	-993-687-37	9-989-73	9-997-65	US-09-993-667-376	9-9	9-166-60-	ı	9-990-562-37	9-990-711-	-72	9-998-156-	ú	19-991-157-3	9-997-514-3	9-997-573-3	US-09-991-172-376	9-990-726-37	9-997-559-37	9-997-601-3	-066-6	-09-991-85	19-997-628-	19-997-683-37	-989-729A-3	19-997-349-3	US-09-997-440-376
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 US-09-989-722-376

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE STATE OF TAXABLE STATE OF TAXABLE SECONDES ACIDS ACID
Sequence 376, Application US/09989722
Patent No. US20020072067A1
PAPPLICANT: Ashkenazi, Avi J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E.
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Gerber, Hanspeter
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Kljavin, Ivar J.
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Godowski, Paul
                                                                                                                                                                                                                                                             Botstein, David
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DR APPLICATION NUMBER: 60/065186

BR FILING DATE: 1997-11-12

BR FILING DATE: 1997-11-13

BR FILING DATE: 1997-11-13

BR APPLICATION NUMBER: 60/066770

BR FILING DATE: 1997-11-24

BR APPLICATION NUMBER: 60/066770

BR FILING DATE: 1998-02-25

BR FILING DATE: 1998-03-20

BR PILING DATE: 1998-03-20

BR PILING DATE: 1998-04-28

BR FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/087759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/087827
FILING DATE: 1938-66-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088030
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION UNDERS: 60/089512
PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-24
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Sequence 376, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy T
Tumas, Daniel
                                                                                                                                                                                          Ferrara, Napoleone
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Paoni, Nicholas F.
                                                                                                                                                                                                             Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                          Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                            Napier, Mary A.
                                                                                                         Baker, Kevin P.
                                                                                                                                                                                                                                                                                             Godowski, Paul
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100.0%; Pred. No. 5e-161;
ive 0; Mismatches 0
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/091544
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PLING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PRILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PRILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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Best Local Similarity 100.
Matches 713; Conservative
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AFFLIANT: Landing, Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/989,723

CURRENT APPLICATION NUMBER: US/049787

PRIOR APPLICATION NUMBER: 60/06150

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-03-04-28

PRIOR PILING DATE: 1998-03-07

PRIOR PILING DATE: 1998-03-07

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PRIOR PILING DATE: 1998-03-07

PRIOR PILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084600

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PRIOR PILING DATE: 1998-05-07 R APPLICATION NUMBER: 60/088028 R FILING DATE: 1998-06-04 R APPLICATION NUMBER: 60/088029 R FILING DATE: 1998-06-04 R APPLICATION NUMBER: 60/088030 R FILING DATE: 1998-06-04 PRIOR

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R APPLICATION NUMBER: 60/090540

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R APPLICATION NUMBER: 60/090676

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R APPLICATION NUMBER: 60/090472
R APPLICATION DATE: 1998-06-24 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/09
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R FILING DATE: 1997-11-24
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
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FILING DAFE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088028
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FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/066770
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FILING DATE: 1998-05-07
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PICS6
CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACAATCATCTTTAGAAGACAG
                                                                                                                                                                                                                                                                                                                        GTATCCCTGTCATATATACAATAAGGTGAAATTATAAGGTACCCTATGCAGTTGGCTGGAC
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                                                                                        241 TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGAGGAGGAATCT
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 376, Application US/09989279 Patent No. US20020072496Al GENERAL INFORMATION:
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Grimaldi,J.Christopher
Gurney,Austin L.
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Watanabe, Colin K.
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Wood, William I.
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Botstein, David
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REPLING DATE: 1998-07-01

RETLING DATE: 1998-07-01

RAPPLICATION NUMBER: 60/091478

RETLING DATE: 1998-07-02

RETLING DATE: 1998-07-02

RETLING DATE: 1998-07-02

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RETLING DATE: 1998-07-02

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RETLING DATE: 1998-07-07 Query Match Best Local Similarity 100. Matches 713; Conservative 481 481 541 601 601 661 661 541 301 61 121 121 181 181 241 241 301 361 421 61 PRIOR
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PRIOR PLILNG DATE: 1998-06-05
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CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PELICATION NUMBER: 60/065111
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065711
PRIOR PELICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/076945
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-26
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08322
PRIOR APPLICATION NUMBER: 60/08360
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
                                                                        Sequence 376, Application US/09989727
patent No. US20020072497A1
patent No. US20020072497A1
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Gurney, Austin L.
Kljavin, Ivar J.
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Stewart, Timothy A.
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ADDITION NIMBED . 60/000355	181 CHITHCHAICABABAADACACACACACACACACACACACACATCATCTTAGAAGACAG 240
φ	181 CTTCTATCAAGAAATAAAGAGAACCACACAACCACCACAATCATCTTTAGAAGACAG
FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24	Qy 241 TGTGACTCCTACCAAAGCTGTCAAAACCACAGGGCAAAGGGCATAGTTAAAGGACGGAATCT 300 Db 241 TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAAGGGCATAGTTAAAGGACGGAATCT 300
AFELING DATE: 1998-06-24 APPLICATION NUMBER: 60/09044 FILING DATE: 1998-06-24	301 TGACTCAAGAGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGTGTAAAGAAAAACACA301 TGACTCAAGAGGGTTAATTCTTGGTGCTGAAGCCTGGGGGGGG
FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535	
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FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676	OY 481 AGTTCTABATTGGACTTTATTAATTTTAAAATCAGTAACTGATTTATCACTGGCTATGT 540
FILLING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090690	OY 541 GCITAGAICTACAGAGATCATATAATTIGATACAAATAAAGAAAGIGITCTCTCCC 600 Db 541 GCITAGATCTACAGGAGATCATATAATTIGATACAAATAAAAGAAAAG
FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/090695	QY 601 TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG 660 Db 601 TTACAGAATTGACATTTTAAATGCGATACAGTTAGAAATATGACAATTAGAAAGG 660
FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862	Oy 661 AAGAATGACAGGGAGAAAGGAAAGGGAAAATGTTGCCAAGGAAAAAAA 713
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FFILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544	
	; APPLICANT: Baker, Kevin P. ; APPLICANT: Botstein, David ; APPLICANT: Desnoyers, Luc ; APPLICANT: Baton, Dan L.
FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/092182	APPLICANT: Ferrara Mapoleone APPLICANT: Fong, Sherman APPLICANT: Gerritsen, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Gurney, Austin I.
PRIOR FILING DATE: 1998-07-09 uery Match est Local Similarity 100.0%; Pred. No. 5e-161; atches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
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Pred. No. 5e-161;
); Mismatches 0
PRIOR FILING DATE: 1998-06-26
PRIOR PAPPLICATION NUMBER: 60/091360
PRIOR PAPPLICATION NUMBER: 60/091470
PRIOR PAPLICATION NUMBER: 60/091470
PRIOR PELLING DATE: 1998-07-01
PRIOR PELLING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091549
PRIOR PAPLICATION NUMBER: 60/091519
PRIOR PAPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091633
PRIOR PAPLICATION NUMBER: 60/091639
PRIOR PELING DATE: 1998-07-07
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Best Local Similarity 100.
Matches 713; Conservative
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APPLICANT: Zhaod, MILLIANI I.

APPLICANT: Zhaod, MILLIANI I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same CITLE REFERENCE: P237081C57

CURRENT PLING DATE: 2001-11-19

PRIOR PLING DATE: 1997-06-16

PRIOR PLING DATE: 1997-06-16

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-13

PRIOR PLING DATE: 1997-11-13

PRIOR PLING DATE: 1997-11-13

PRIOR PLING DATE: 1999-04-29

PRIOR PLING DATE: 1999-06-04

PRIOR PLING DATE: 1990-06-04

PRIOR PLING DATE: 1990-06-04
; Sequence 376, Application US/09989732; Patent No. US20020123463A1; GENERAL INFORMATION:
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FILING DATE: 1998-06-04
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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                                                                                                           APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
                                                                                                                                                                                         Botstein, David
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Eaton, Dan L.
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APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 APPLICATION NUMBER: 60/08861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
APPLICATION NUMBER: 60/088824
APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 ILING DATE: 1998-06-17 PPLICATION NUMBER: 60/089599 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089514 APKLLAND DATE: 1998-06-03
APPLICATION NUMBER: 60/088033
APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 APPLICATION NUMBER: 60/088738 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-19 1998-06-22 1998-06-17 FILING DATE: 1998-06-18 LING DATE: 1998-06-16 1998-06-18 1998-06-22 1998-06-10 1998-06-17 1998-06-05 1998-06-05 1998-06-10 1998-06-05 LING DATE: 1998-06-APPLICATION NUMBER: ILING DATE: LING DATE: LING DATE: FILING DATE: FILING DATE: FILING DATE: LING DATE: PRIOR PRIOR

121 GIIGGIAIGIGAAGCIAÍTIGGAGAICCAAIICAGGAAGCAAGCACACIIGGAGAAIGGCIA 180 TITICGGATITITAATITITCAAACACAGCAGAATGACATITITITICIGICACTATIATIT 120 GITGGIATGIGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180 1 AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG 1 AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG ; 0 Length 713; Indels 100.0%; Score 713; DB 9; 100.0%; Pred. No. 5e-161; Mismatches APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090678 ; 0 1998-07-02 FILING DATE: 1998-07-07 1998-06-24 1998-06-24 1998-06-25 1998-06-25 FILING DATE: 1998-06-25 FILING DATE: 1998-07-02 1998-06-24 Query Match 100. Best Local Similarity 100. Matches 713; Conservative FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: 61 121 PRIOR
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                  241 TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT 300
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CTTTCTATCAAGAAATAAAGAAACCACAGACCCACACAATCATCTTTAGAAGACAG
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Grimaldi, J. Christopher
Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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Eaton, Dan L.
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR PLING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-12
PRIOR PLICATION NUMBER: 60/065311
PRIOR PLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1998-02-25
PRIOR PLING DATE: 1998-02-27
PRIOR PLING DATE: 1998-06-07
PRIOR PRICATION NUMBER: 60/08815
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R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090435
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R APPLICATION NUMBER: 60/090444
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R APPLICATION WNMBER: 60/089952
R FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/990696
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APPLICATION NUMBER: 60/090862
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/089948
FILING DATE: 1000
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/089599
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089514
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99 099 480 540 540 600 600 180 300 360 360 420 420 480 09 GTATCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGGAAAAGTGTTCTCTCCCC TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG GCTTAGATCTACAGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCC GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA CTTTCTATCAAGAAATAAAGAGGAACCACAGTCAACCCCACACAATCATCTTTAGAAGACAG rgacricaagagggrinarrichtggrgcrgaagccrggggggggggggggggaaaagaaaacac 361 TIAGATTCAATGATTGTAAATTTAAGGCAATACACATATTAGTATTACCTTAGTGTAAT 481 AGTICTAAATTGGACTTTATTAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGT 1 AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG 1 AATATATCATCATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT rgrgacrccraccaaagcrgrcaaaaccacaggcaagggcaragrraaaggacggaarcr TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT **AGTICTAAATTGGACTTTATTAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGT** Gaps 713 0; 0; Indels 100.0%; Score 713; DB 9; ilarity 100.0%; Pred. No. 5e-161; Conservative 0; Mismatches 0; R APPLICATION NUMBER: 60/091360
R APPLICATION NUMBER: 60/091360
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R APPLICATION NUMBER: 60/091633
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/091626 60/090863 FILING DATE: 1998-07-07 APPLICATION NUMBER: Query Match Best Local Similarity Matches 713; Conserv 481 541 541 601 109 181 241 241 301 301 361 421 121 181 61 61 PRIOR
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PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
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PRIOR PAPLICATION NUMBER: 60/088032
PRIOR PAPLICATION NUMBER: 60/088026
PRIOR APPLICATION NUMBER: 60/088020
PRIOR APPLICATION NUMBER: 60/088020
PRIOR PILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/088012
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PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089518
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PRIOR PILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/08994
PRIOR PILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/099801
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CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-13

PRIOR PELING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/06531

PRIOR APPLICATION NUMBER: 60/075945

PRIOR PILING DATE: 1998-02-25

PRIOR PELING DATE: 1998-02-26

PRIOR PILING DATE: 1998-04-28

PRIOR PELING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087607

PRIOR PELING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087607

PRIOR PELING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087607

PRIOR PELING DATE: 1998-06-02

PRIOR PELING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR PELING DATE: 1998-06-02

PRIOR PELING DATE: 1998-06-02
                                                                                                      Sequence 376, Application US/09990442
Patent No. US20020132252A1
GENDERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088029
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
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Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
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US-09-990-442-376
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GITGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273-091C17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
                                                                                                                                        TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT
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                                               CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCACACAATCATCTTTAGAAGACAG
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Patent No. US20020132253A1
GENERAL INFORMATION:
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Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
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100.0%; Pred. No. 5e-161;
iive 0; Mismatches 0
                      PRIOR FILING DATE: 1998-06-23
PRIOR PLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090439
PRIOR PLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PRIOR DATE: 1998-06-26
PRIOR PRIOR DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATIO
         60/090349
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088033
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R APPLICATION NUMBER: 60/088326
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R APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212 R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088030 R APPLICATION NUMBER: 60/087609
PR FILING DATE: 1998-06-02
PR APPLICATION NUMBER: 60/08759
PR FILING DATE: 1998-06-02
PR APPLICATION NUMBER: 60/087827
PR ILING DATE: 1998-06-03
PR ILING DATE: 1998-06-03
PR APPLICATION NUMBER: 60/088021 R FILING DATE: 1998-04-28

A APPLICATION VUMBER: 60/084600

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/087106

R FILING DATE: 1998-05-28

R PILING DATE: 1998-06-07

R FILING DATE: 1998-06-02 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILLING DATE: 1998-06-11 APPLICATION NUMBER: 60/088861 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
ALING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026 FILING DATE: 1998-02-25
APPLICATION UNMBER: 60/078910
ALING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/065186 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13 1998-06-10 1998-06-11 1998-02-25 FILING DATE: 1997-06-16 FILING DATE: PRIOR PRIOR

PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/089514
PRIOR PLING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR PLING DATE: 1998-06-17
PRIOR PRILING DATE: 1998-06-17
PRIOR PRILING DATE: 1998-06-17
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PRIOR PELICATION NUMBER: 60/08959
PRIOR PLING DATE: 1998-06-17
PRIOR PELICATION NUMBER: 60/08960
PRIOR PLING DATE: 1998-06-17
PRIOR PELICATION NUMBER: 60/08961
PRIOR PELICATION NUMBER: 60/08961
PRIOR PLING DATE: 1998-06-18
PRIOR PELICATION NUMBER: 60/08961
PRIOR PLING DATE: 1998-06-18
PRIOR PELICATION NUMBER: 60/08961
PRIOR PLING DATE: 1998-06-19
PRIOR PELICATION NUMBER: 60/09048
PRIOR APPLICATION NUMBER: 60/09048
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
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661 AAGAATGACAGGGAGAAAGGAAAGGAAAATGTTGCCAAGGAAAAAAA 713
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APPLICATION NUMBER: 60/088028
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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US-09-993-604-376
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Pred. No. 5e-161;
; Mismatches 0;
                            PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091860
PRIOR APPLICATION NUMBER: 60/091470
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/092182
                   60/090862
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Best Local Similarity 100.
Matches 713; Conservative
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/993,604
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-06-02
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PRIOR PILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-03
Sequence 376, Application US/09993604 Patent No. US20020137075A1
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Roy, Margaret Ann
Stewart, Timchy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Gerritsen, Mary 3.
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Godowski, Paul J.
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PRIOR FILING DATE: 1938-06-04

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PRIOR PRING DATE: 1938-06-05

PRIOR PILING DATE: 1938-06-05

PRIOR PILING DATE: 1938-06-05

PRIOR PELICATION NUMBER: 60/08812

PRIOR PILING DATE: 1938-06-05

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PRIOR PELING DATE: 1938-06-05

PRIOR PELICATION NUMBER: 60/088217

PRIOR PELING DATE: 1938-06-05

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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090246
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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TTTTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTTTTCTGTCACTATTATTATT 120 121 GITGGTAIGTGAAGCIAITTGGAGAICCAATICAGGAAGCAACACATIGGAGAAIGGCIA 180 1 AATATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACAATTTGGG 61 irridesarriraarrircaaacacagcagaargacarrirrircrorcacrarrarr 1 AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG Gaps Length 713 Indels Score 713; DB 9; Pred. No. 5e-161; 0; Mismatches 0; APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 PILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091978 FILLING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 CATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 069060/09 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 100.0%; 100.0%; FILING DATE: 1998-07-02 FILING DATE: 1998-07-07 1998-06-25 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ 1998-06-24 FILING DATE: 1998-06-25 1998-06-25 1998-06-25 FILING DATE: 1998-07-01 FILING DATE: 1998-06-24 1998-06-24 Query Match 100. Best Local Similarity 100. Matches 713; Conservative APPLICATION NUMBER: FILING DATE: 1998-06 FILING DATE: FILING DATE: FILING DATE: FILING DATE: 61 PRIOR ð 셤 ð g à

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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Napier, Mary A.
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Botstein, David
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PILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088824
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APPLICATION UNMBER: 60/088028
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087609
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/049787
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APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 APLING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 APLING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
FILING DATE: 1998-06-22 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 LING DATE: 1998-06-12 PLICATION NUMBER: 60/089440 PLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-25 1998-06-24 1998-06-24 1998-06-24 1998-06-18 1998-06-17 FILING DATE: FILING DATE: LING DATE: FILING DATE: PRIOR PRIOR

099 099 009 600 420 480 480 300 300 9 TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATAGGAATTGACATTAGAAAGG 541 GCTTAGATCTACAGGAGGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCC 181 CTTTCTATCAAGAAATAAAGAGAAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG TGACTCAAGAGGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACAC reacticaacacicaatrictrectecteaaccerececacecacecritaaacaacac TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT TIAGATICAAIGATIGIAAATITAAGGCAAAIACACATAITAGTATIACTATIAGTGTAAT GTATCCCTGTCATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC GIATCCCIGICATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC **AGTICTAAATTIGGACTITIATTAATTITTAAAATCAGTAACTGATTTATCACTGGCTATGT** rdrgacriccraccaaagcrdrcaaaaccacaagggcaragrraaaggacgaarcr CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT 1 ANTARCARCIATITATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG TITIGGGATITITAATITITCAAACACAGCAGAATGACATITITITITITICAGTATTATTATT GITGGIAIGIGAAGCIAITIGGAGAICCAAITCAGGAAGCAACACAITGGAGAAIGGCIA Gaps .. 0 Length 713; Indels 100.0%; Score 713; DB 9; 100.0%; Pred. No. 5e-161; ive 0; Mismatches 0; PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR APPLICATION NUMBER: 60/090863
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/091544
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09193
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 Query Match Best Local Similarity 100. Matches 713; Conservative 601 241 481 541 241 301 301 361 361 421 421 61 61 121 181 음 ò à g g δ 셤 8 g ð Š ò 셤 ð g à 임

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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR PLING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-05
PRIOR PELICATION NUMBER: 60/088126
PRIOR PELING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-12
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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APPLICANT: MOOG, MILLIAM 1.

APPLICANT: MOOG, MILLIAM 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: P2130P1C55

CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT PELING DATE: 1997-10-13

PRIOR FILING DATE: 1997-10-14

PRIOR PLING DATE: 1997-10-12

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1998-02-25

PRIOR PLING DATE: 1998-02-25

PRIOR PLING DATE: 1998-02-25

PRIOR PLING DATE: 1998-02-26

PRIOR PLING DATE: 1998-02-07

PRIOR PLING DATE: 1998-06-07

PRIOR PRIOR PLING NUMBER: 60/080026

PRIOR PLING DATE: 1998-06-07

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PRIOR PRIOR PLING NUMBER: 60/080026

PRIOR PRIOR PLING NUMBER: 60/080026

PRIOR PLING DATE: 1998-06-04

PRIOR PLING DATE: 1998-06-04
                                                     Sequence 376, Application US/09989721 Patent No. US20020142961A1 GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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                                                                                                                                                         RESULT 12
US-09-989-721-376
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GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Actids Encoding the Same
FILE REFERENCE: P2730PlC20
                                                                                                                              CITICIATORAGAAATAAAGAGAAACACACACACCACACAATCATCATCATTAGAAGAAGAGAG
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                                         GTIGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACTTGGAGAATGGCTA
                                                                                          CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG
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Grimaldi,J.Christopher
Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Eaton, Dan L.
Ferrara, Napoleone
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Goddard, Audrey
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Paoni, Nicholas F.
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Botstein, David
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Patent No. US20020160384A1
GENERAL INFORMATION:
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US-09-992-598-376
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APPLICANT:
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100.0%; Pred. No. 5e-161;
cive 0; Mismatches 0,
                                         PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-24
PRIOR PRIOR DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090659
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PRIOR DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09169
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PRIOR DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-07
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         APPLICATION NUMBER: 00, 177 FILLNG DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 1998-06-22 APPLICATION NUMBER: 00/090355
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR PLILICA DATE: 1997-06-16
PRIOR PLILICA DATE: 1997-11-12
PRIOR PLILICA DATE: 1997-06-16
PRIOR PLILICA DATE: 1997-06-17
PRIOR PLILICA DATE: 1997-06-17
PRIOR PLILICA DATE: 1997-06-17
PRIOR PLILICA DATE: 1997-06-17
PRIOR PLILICA DATE: 1998-06-20
PRIOR PREDICATION NUMBER: 60/08021
PRIOR PLILICA DATE: 1998-06-20
PRIOR PLILING DATE: 1998-06-20
PRIOR PRIOR PLILING DATE: 1998-06-10
PRIOR PRIOR PLILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-11
PRIOR PRING APPLICATION NUMBER: 60/08940
PRIOR PELLING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PELLING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-17
PRIOR PELLORICATION NUMBER: 60/08907
PRIOR PELLING DATE: 1998-06-17
PRIOR PELLORICATION NUMBER: 60/08904
PRIOR PELLING DATE: 1998-06-18
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PRIOR PELLING DATE: 1998-06-18
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PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-25
PRIOR PELLING DATE: 1998-06-25
PRIOR

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLLE OF INVENTION: Acids Encoding the Same
                                   FILE REFERENCE: P2730P1066
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06710
PRIOR PILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-00
PRIOR PLING DATE: 1998-04-28
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: 60/08460
PRIOR APPLICATION NUMBER: 60/08460
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08760
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PRIOR APPLICATION NUMBER: 60/087769
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RRIOR APPLICATION NUMBER: 60/08727
PRIOR FILING DATE: 1998-06-03
RRIOR APPLICATION NUMBER: 60/088021
PRIOR PILING DATE: 1998-06-04
RRICR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
                                                                                                                                                 Sequence 376, Application US/09989293A Patent No. US20020177164A1 GENERAL INFORMATION:
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/049787
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APPLICATION NUMBER: 60/062250
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Godowski, Paul J.
Grimaldi, J.Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleone
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Kljavin, Ivar J.
Napier, Mary A.
Pan, James
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                 Botstein, David
                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                           Baker, Kevin P.
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APPLICANT:
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100.0%; Score 713; DB 9;
Best Local Similarity 100.0%; Pred. No. 5e-161;
Matches 713; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
                                                                                                                                        APPLICATION NUMBER: 60/091360
FILING DATE: 1996-07-01
APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
                                   FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
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FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/086030
PRIOR PLING DATE: 1998-06-04
PRIOR PRIOR DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-17
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PRIOR PRILING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/088028

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PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090359
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PRIOR FILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-27
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-03
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US/09/989,735
                                                           PRIOR AFFILCATION NUMBER: 60/06250
PRIOR PRIOR PLING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
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PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-07
PRIOR PELICATION NUMBER: 60/08012
PRIOR PELICATION NUMBER: 60/08012
PRIOR PELICATION NUMBER: 60/08013
PRIOR PELICATION NUMBER: 60/08013
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CURRENT APPLICATION NUMBER: US/09/90
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PRIOR APPLICATION NUMBER: 60/049787
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-11
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Thang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA
                                                                                        CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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Search completed: April 4, 2004, 08:05:41 Job time: 413 secs

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Query Match 10.9%; Score 77.6; DB 3; Length 2298; Best Local Similarity 73.1%; Pred. No. 8.5e-11; Matches 114; Conservative 0; Mismatches 39; Indels 3.
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Sequence 1, Appli
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Sequence 651, App
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Sequence 45,
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Sequence 4,
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/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 1, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
    APPLICANT: Ariizumi, Kiyoshi
    APPLICANT: Takashima, Akira
    TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
    TITLE OF INVENTION: TREREOF
    NUMBER OF SEQUENCES: 42
    CORRESPONDENCE ADDRESSE:
    CORRESPONDENCE ADDRESSE:
    STREET: P.O. Box 4433
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83, Appl
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            Sequence 10,
Patent No. 542
Sequence 2, A
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Sequence 11
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Sequence 2
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MEDITUM TYPE: Floppy disk
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: PRAFE. David L.
US-09-097-319A-9
US-09-097-319A-10
US-10-204-708-2
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US-10-204-708-14
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US-10-204-708-14
US-10-204-708-14
US-10-204-708-14
US-10-204-708-14
US-10-204-708-14
US-09-165-313
US-09-256-075-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /\text{note} = "Y = C \text{ or } T"
                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERNICE/DOCKET NUMBER: UTXD:493
TELEPHONE: 512/418-3000
TELEPAN: 512/418-3000
TELEPAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2298 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1966
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "Y = C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2298 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified base
                                                                                                                                      3331
161652
6113
6317
11050
50000
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2570
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24595
10467
19124
10640
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51952
408
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STATE: Texa.
COUNTRY: USA
T7210
    STREET: P.O. E
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APPLICANT: Aritumi, Kiyoshi
APPLICANT: Takashima, Akira
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 TTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATA 197
                                                                                                                       334 CAACTICCIAICAAGAAAIAAAGAGAACCACA---AGCCCACAGAAICAICTIIAGAIGA 390
                                       118 ATTGTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAATGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 AAGAGAACCACAGTCAACCCACACACATCTTTTAGAAGACAGTGTGACTCCTACCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ririgeceacacaarircaeegagaaarecaeaegagagaaagacaacrirecrarcaagaara
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Pred. No. 2.3e-10;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: TEXAS

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLESSIFICATION: 4355
                                                                                                                                                                      238 CAGTGTGACTCCTACCAAAGCTGTCAAAACCACAGG 273
                                                                                                                                                                                                              391 GAAGGTGGCTCCCTCCAAGGCATCCCAAACTACAGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08772440 Patent No. 6046158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCCCAAACTACAGG 134
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
IENGTH: 528 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.5
Best Local Similarity 77.2
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
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                                                                                    178
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553 AGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGA 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46.6; DB 1; Length 7218; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 GAGAAAGGAAAGGGAAAATGTTGCCAAGGAAAAAAA 713
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-08-232-463-14/c
| Sequence 14, Application US/08232463
| Patent No. 5670367
| GENERAL INFORMATION:
| APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: RALKNER, F. G. APPLICANT: RALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY, AGGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: John St. S.
                                                                                                                                                                                                                 SSEE: Foley & Lardner
F: 1800 Diagonal Road,
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14.
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%;
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-621-976-2813
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES: 1059.04.1,638
CURRENT FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
PRIOR PLICATION NUMBER: US 60/133,200
PRIOR PLICATION NUMBER: US 60/133,200
PRIOR PLING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-21
PRIOR FILING DATE: 1999-03-21
SPIOR FILING DATE: 1999-03-22
SPIOR PLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-23
SPIOR PLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-23
SPIOR PLICATION NUMBER: US 60/119,917
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                                                                                                                               Sequence 10, Application US/09920672

Patent No. 645308

GENERAL INFORMATION:
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
FILE REPRERENCE: RTS-0281
CURRENT APPLICATION NUMBER: US/09/920,672
CURRENT APPLICATION NUMBER: US/09/920,672
CURRENT PILING DATE: 2001-08-01
SEQ ID NOS: 89
LENGTH: 5847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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117629 TGATGGGATTAGTCTCACTGTCAATGATATTAATAAAATGAAT 117672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 40.4; DB 4;
ilarity 68.3%; Pred. No. 0.41;
Conservative 0; Mismatches 26;
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OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1144 GGAGAAAGAAAGAAAAGGAAAA 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 651, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               692 AATGTTGCCAAGGAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 3124..3297
OTHER INFORMATION: exon 1
NAME/KEY: exon
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LOCATION: 1123.3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 3871..4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20674
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                                                                                                  RESULT 6
US-09-920-672-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
US-09-920-672-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117569 GTTAAAAATGAATAATATGTCTTTAATGAAGTATATTTTCTATAAAGGATTTATATCTGTGT 117628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 CTGGACAGIICTAAATIGGACTITAITAATITITAAAAICAGIAACTGAITTAICACTGG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 KAWITWWWKKIYYWAATRYWWMCWIKRWRASWWYCWWWGKARKWSTWRKSRSYASARSA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 KRCCYSCSWGAMSWKYMRWRRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYKSMMCW 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 GATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-CTAAATTGGACTTTATTAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 TGTAATGTATCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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54.3%; Pred. No. 0.19;
ative 0; Mismatches 75; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SARAKI, YOSHIYUKI
TITLE OF INVENTIORI GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/01.59
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR TELING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQIED NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 45.2; DB 4; Length 832;
17.4%; Pred. No. 0.014;
tive 108; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535 CTATGTGCTTAGATCTACAGGAGATCATATAATTTGATACAAAT 578
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENEST. 0.54PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 2813
LENGTH: 932
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 17.4%; Prec. No.
Best Local Similarity 17.4%; Prec. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09790988
Patent No. 6632935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.3
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.1
                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Buchnera sp.
                                                                                                                                                                                                                                                                                                                            ; LOCATION: 235..399
US-09-621-976-2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 640681
                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-790-988-1
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                                                                                                                                                                                                                              TYPE: DNA
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: variable motif ATTTA or TTTTT
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LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
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LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 1570
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATI
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: exon 14
MAME/KEY: misc. feature
LOCATION: 17555_.20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 1182
COTHER INFORMATION: 10-508-245 :
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COCATION: 1128
THER INFORMATION: 10-508-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOCATION: 16567..16667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 12854..13023
OTHER INFORMATION: exon 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ION: 16775..16945
INFORMATION: exon 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION: exon 11
OTHER INFO...
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
                                                                                                                                                                                                                                                                                                                                                                                                          ION: 12254..12340
INFORMATION: exon 9
                                                                                    NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
                                                                                                                                                                                                                             LOCATION: 6349..6509
OTHER INFORMATION: exon 6
                                                                                                                                                                                   OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: exon 7
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T.OCATION: 17063..17554
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OTHER INFORMATION: 10-313-231 . GETELLIN OF STATES OF STATES OTHER INFORMATION: 12-206-366 : polymorphic base C or T NAME/KEY: allele  
LOCATION: 4109  
OTHER INFORMATION: 10-343-278 : polymorphic base C or T NAME/KEY: allele  
LOCATION: 4170  
OTHER INFORMATION: 10-343-339 : polymorphic base G or T NAME/KEY: allele  
LOCATION: 5903  
OTHER INFORMATION: 10-346-23 : polymorphic base A or G NAME/KEY: allele  
LOCATION: 6019  
OTHER INFORMATION: 10-346-141 : polymorphic base A or G NAME/KEY: allele  
LOCATION: 6019  
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-271 : polymorphic base A or G
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
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LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
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                                                                                                                                                                                          : polymorphic base A or G
LOCATION: 2934

OTHER INFORMATION: 10-513-352 : polymorphic base A or of NAME/KEX: allele
LOCATION: 294

OTHER INFORMATION: 10-513-365 : polymorphic base A or LOCATION: 3802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 6141
STHER INFORMATION: 10-346-263 : polymorphic base G or
NAME/KEY: allele
COCATION: 6183
STHER INFORMATION: 10-346-305 : polymorphic base C or
NAME/KEY: allele
LOCATION: 6338
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                                                                                                                                                                                                                                                                           : deletion of C
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LOCATION: 7668
LOCATION: 7668
LOCATION: 8608
LOCATION: 8608
CTHER INFORMATION: 10-349-47 : F
NAME/KEX: allele
LOCATION: 8658
CTHER INFORMATION: 10-349-97 : F
NAME/KEX: allele
LOCATION: 8703
CTHER INFORMATION: 10-349-97 : F
NAME/KEX: allele
LOCATION: 8703
CTHER INFORMATION: 10-349-142 : NAME/KEX: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 8777
OTHER INFORMATION: 10-349-216
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LOCATION: 6611
OTHER INFORMATION: 10-347-348
                                                                                                                                                             LOCATION: 3802
OTHER INFORMATION: 12-206-81
NAME/KEY: allele
LOCATION: 4662
OTHER INFORMATION: 10-343-231
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424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             655 AAAATTTACATATGAAAATGAACTTGTATATGTAAATTTAAAATATTTTAAACATAAA 714
                                                                                                                                                                                                                                                                                                                                              478 AACCAICCIATATATATACACAATATATAATACICCCCAATATTGIGGITCCTATAATT
                                                                                                                                                                                                                                                                                                                                                                                          485 CTAAATTGGACTTTATTAAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTT
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                                                                                                                                                                                   Gaps
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TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
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                                                                                                                                         Length 8920;
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                                                                                                                                                                                 0; Mismatches 183; Indels
                                                                                                                                       Score 39.2; DB 2;
Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER APLICATION NUMBER: AU93/00617
EARLIER APLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09150741
Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1
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                                                                                                                                         Query Match 5.5%;
Best Local Similarity 46.6%;
Matches 162; Conservative
  LENGTH: 8920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 162; Conservative
                                                       ; TOPOLOGY: linear; MOLECULE TYPE: genomic US-08-446-855A-1
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Best Local Similarity
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US-09-150-741-1
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 20674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
APPLICANT: Stewart, Thomas S
APPLICANT: O'SULLYAN, William J
APPLICANT: O'SULLYAN, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels
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                       : polymorphic base C or
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                                                                                    or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Nixon & Vanderhye PC
: 1100 No. 5849573th Glebe Road, 8th Floor
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                  : polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.6; DB
Pred. No. 0.96;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISCRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                            OTHER INFORMATION: 10-507-321
OTHER INFORMATION: 10-507-321
LOCATION: 8926
OTHER INFORMATION: 10-349-368
NAME/KEY: allele
                                                                                               NAME/KEY: allele
LOCATION: 12429
OTHER INFORMATION: 10-350-332
                                                                                                                                                            NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170
                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 10-507-353
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.0%;
Matches 75; Conservative
                                                             LOCATION: 12171
OTHER INFORMATION: 10-350-72
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                                                                                                                                                                                                                                                         OTHER INFORMATION NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 13535
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US-08-446-855A-1
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STATE:
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1928 TTAACTGATCATAAATTTTAAAAAAAAGATGAATTATGT 1888
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                                    551 ACAGGAGATCATATAATTTGATACAAATAAAAGAAAGTGT
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                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828 CITY: Troy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word for Windowe-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,887A
FILING DATE: September 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 75550001USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                                     US-08-308-887A-4/C
; Sequence 4, Application US/0830887A
; Parent No. 5883076
; GENERAL INFORMATION:
APPLICANT: Ryan, C.A.
APPLICANT: McGurl, B.F.
APPLICANT: Pearce, G.L.
; TITLE OF INVENTION: "SYSTEMIN"
NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch,
COMPUTER: IBM FO/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
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Best Local Similarity 48.4%;
Matches 107; Conservative (
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TELEX: 287637 Harnes UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Michigan
COUNTRY: USA
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                                                                            545 AGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTAC 604
                                    538 TTATTTATATTTTATTTATTTATTCATTTATTTATTTT---TTTCTTAGTTTAT
                                                                                                                   605 AGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGA
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485 CTAAAITGGACTTTATTAAITTTTAAAATCAGTAACTGATTTAICACTGGCTAIGIGCTT
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                                                                                                                                                                                                                                                                             Length 4526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
DESCRIPTION: prosystemin genomic DNA; Figures 8A-8C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2Mb storage
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                                                                                                                                                                                                                                                                                                                                                              US-07-855-412B-4/c
; Sequence 4, Application US/07855412B
; Patent No. 5378B109;
GENERAL INFORMATION;
APPLICANT: Ryan,C.A.;McGurl,B.F.;Pearce,G.L.;
IITLE OF INVENTION: "SYSTEMIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
5.4%; Score 38.6;
Best Local Similarity 48.4%; Pred. No. 1.:
Matches 107; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Harness, Dickey & Pierce STREET: P.O. Box 828
CITY: Troy
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RR: 755500002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36,6
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TELEX: 287637 Harnes UR
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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N: 536
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APPLICATION NUMBER: US
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STRANDEDNESS: single
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US-07-855-412B-4
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LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                           346 TGTAAAGAAAAACACTTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTA 405
                                                                                                                                                                                                                                                                               700 TATGAAATATCCCCTTTCAAACAATTAGATGTTAATAAAGGAAAGCTCAAAAATCAATT 759
                                                                                                                                                                                                                                                                                                                                       406 TTACCTTAGTGTAATGTATCCCTGTCATATATAAGGTGAAATTATAAGTACCCTA 465
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Patent No. 667731

GENERAL INFORMATION:

APPLICANT: DIEK, Alexander

APPLICANT: PIEPENBROCK, Christian

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: by Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT BILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: PCT/EP01/03971
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OTHER INFORMATION: n is a or g or c or t
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                                                                                                                                                                            Gaps
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                                                                                                                 Length 58407;
                                                                                                                                                                      Indels
                                                                                                                 DB 4;
                                                                                                                                                                0; Mismatches 126;
                                                                                                              Score 38.4; Di
Pred. No. 2.6;
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; LOCATION: (6485)..(6485); OTHER INFORMATION: n equals a, t, c, or g US-08-916-421B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PRIING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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                                                                                                            Query Match 5.4%;
Best Local Similarity 47.5%;
Matches 114; Conservative
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LENGTH: 19233
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US-10-204-708-45
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GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729

TITLE OF INVENTION: januaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
FUNR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428

PRIOR APPLICATION NUMBER: US 60/024,428

PRIOR SEQ ID NOS: 3

SOFTWARE PATENT NOS: 3

SOFTWARE PATENT NOS: 3

SOFTWARE PATENT NOS: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1988 TGAACATAAAATTTTTAAAAAAAAATAGATGACTTATGTACGAGCAAAATTGTATATAAAAGT 1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.4%; Score 38.6; DB 3; Length 4526; Best Local Similarity 48.4%; Pred. No. 1.1; Matches 107; Conservative 0; Mismatches 114; Indels 0
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                                                                                       GENERAL INFORMATION:
APPLICANT: Ryan, Clarence A
APPLICANT: Ryan, Clarence A
APPLICANT: Ryan, Clarence A
APPLICANT: Rearce, Gregory L
APPLICANT: Mcdurl, Barry E
TITLE OF INVENTION: Systemin
FILE REFERENCE: 7555-00001CPB
CURRENT FILING DATE: 1997-07-09
BARLIER APPLICATION NUMBER: 08/308,887
EARLIER APPLICATION NUMBER: 08/308,887
BARLIER APPLICATION NUMBER: 07/593/02428
BARLIER FILING DATE: 1993-03-19
BARLIER FILING DATE: 1992-03-19
BARLIER FILING DATE: 1992-03-19
BARLIER FILING DATE: 1990-05-25
BARLIER FILING DATE: 1990-05-25
BARLIER FILING DATE: 1991-05-24
NUMBER OF SEQ ID NOS: 43
                                           Sequence 4, Application US/08881094A Patent No. 6022739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Lycopersicon esculentum US-08-881-094-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                               295 GAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAA 354
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                                                                                                                                           Pred. No. 1.3;
0; Mismatches 172; Indels
                                                                                                                     DB 4;
                                                                                                                   Score 37.8;
Pred. No. 1.
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                                                                                                                                                                 Matches 141; Conservative
                            TYPE: DNA
ORGANISM: Sus scrofa
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Job time : 114 secs
                                                                                                                 Query Match
Best Local Similarity
                                                                 US-09-626-959D-2
       LENGTH: 1537
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LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)
OTHER INFORMATION: n is a or g or c or t
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OTHER INFORMATION: n is a or g or c or t
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INFORMATION: n is a or g or c or t
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LOCATION: (4298, 4363, 4610, 4627, 4695, 4698, 4738, 4777, 4781)
OTHER INFORMATION: n is a or g or c or t
                                                                                         5462, 5494, 5496, 5500, 5674)
                                                                                                                                                                                                                                                                        LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)
OTHER INFORMATION: n is a or g or c or t
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OTHER INFORMATION: n is a or g or c or t
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                                                                                    LOCATION: (4787, 4825, 4829, 4838, 4855, OTHER INFORMATION: n is a or g or c or t FEATURE:
                                                                                                                                                                                  LOCATION: (5690, 5697, 5705, 5715, 5890, OTHER INFORMATION: n is a or g or c or t
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Pred. No. ;
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OTHER INFORMATION: n is a or g or c or
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Best Local Similarity
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LOCATION: (10005,
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LOCATION: (19200
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APPLICANT: Findlay, Robert
TITLE OF INVENTION: MYOSTATIN REGULATORY REGION, NUCLEOTIDE SEQUENCE DETERMINATION AN
FITLE OF INVENTION: METHODS FOR ITS USE
FILE REFERENCE: PC10448A
CURRENT APPLICATION NUMBER: US/09/626,959D
CURRENT APPLICATION NUMBER: US/09/626,959D
PRIOR PRIOR PLING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0

Sequence 2, Application US/09626959D Patent No. 6617440 GENERAL INFORMATION:

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April 4, 2004, 04:03:10; Search time 462 Seconds (without alignments) 6556.202 Million cell updates/sec
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES B ID Description		3 AAC58634 Aac58634 Human Pi	0	AAF4240 Aaf44240	ABX77952 Human	7 ABX80364 Abx80364 Novel h	0	7 ACD24089 Acd24089 Novel h	ABX90341 Abx90341	7 ABX64187 Abx64187 cDNA end	7 ACA67230 Aca67230 cDNA end	7 ACA64409 Aca64409 Novel h	7 ACA03839 Aca03839 cDNA en	ABX89377 DNA e	7 ABX80868 Human se		7 ACD42031 Human 8	7 ABX79548 Human s	7 ACA93569 Aca93569 Novel hi	1 Novel	7 ACA04260 Human cl	7 ACA93067 Aca93067 Novel hi
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ALIGNMENTS

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PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1996; 98US-0088825P.
PR 11-JUN-1996; 98US-0088825P.
PR 11-JUN-1996; 98US-0088825P.
PR 11-JUN-1996; 98US-0088825P.
PR 11-JUN-1996; 98US-0089440P.
PR 12-JUN-1996; 98US-0089440P.
PR 12-JUN-1996; 98US-0089532P.
PR 17-JUN-1996; 98US-0089532P.
PR 17-JUN-1996; 98US-0089532P.
PR 17-JUN-1996; 98US-0089532P.
PR 17-JUN-1996; 98US-0089532P.
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PR 17-JUN-1996; 98US-0089532P.
PR 12-JUN-1996; 98US-0089532P.
PR 22-JUN-1996; 98US-0089532P.
PR 22-JUN-1996; 98US-0089532P.
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PR 22-JUN-1996; 98US-0089532P.
PR 22-JUN-1996; 98US-0089532P.
PR 22-JUN-1996; 98US-0089532P.
PR 22-JUN-1996; 98US-0089532P.
PR 22-JUN-1996; 98US-0089532P.
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including IDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane-bound proteins and related nucleotide sequences.
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Wood WI, Yuan J;
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AAC58634 standard; cDNA; 713 (first entry) 29-JAN-2001 AAC58634; RESULT 2 AAC58634

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Human PRO1159 protein UNQ589 encoding cDNA SEQ ID NO:272.

Human, immune related disease, diagnosis, antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; nootropic, neuroprotective; antianaemic; hepatotropic, virucide, antipsoriatic, antialergic; antiathmatic; systemic lupus erythematosus; rheumatoid arthritis; ostemic lupus erythematosus; rheumatoid arthritis; diopathricis; spondyloarthropathy; systemic sclerosis; sarcoidosis; diopath; cinflammatory myopathy; slogren's syndrome; thyroiditis; systemic vacultitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaemia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Mhipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; mutoimmune disease; immune-mediated skin disease; allergic disease; munoidiated skin disease; allergic disease; munoidiated skin disease; allergic disease; munoidiated skin disease; allergic disease; munoidiated skin disease; allergic disease; musuological disease; transplantation associated disease;

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26-APR-1999;
04-MAY-1999;
14-MAY-1999;
23-JUN-1999;
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(GETH) GENENTECH INC.

Henzel W; Gurney AL, Hebert C, He D, Shelton DL, Smith V; Nood WI, Yan M; KP, Goddard A, Gurney AI
Pan J, Pennica D, Sheltc
, Watanabe CK, Wood WI, Ashkenazi AJ, Baker KP, Tumas D, Lu Y, Kabakoff RC, Stewart TA,

WPI; 2000-572271/53.

P-PSDB; AAB33469.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 23; Fig 111; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-bodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematcosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and

Human cDNA sequence encoding for PRO1159 polypeptide

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peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allerglic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACS8397 to AACS8578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS8579 to AACS8642 and AAB33414 to AAB33477 represent human PRO polynucleocide and protein sequences given in the exemplification of the present invention
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AAS21480 standard;

RESULT 3 AAS21480 (first entry)

24-OCT-2001 AAS21480;

EXAXEX XAXEX

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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
rt TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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02-DEC-1999; 99W0-US028651.
02-DEC-1999; 99W0-US028551.
02-DEC-1999; 99W0-US028551.
03-DEC-1999; 99W0-US028564.
04-DEC-1999; 99W0-US0303019.
05-DEC-1999; 99W0-US0303019.
05-DEC-1999; 99W0-US030099.
06-JAN-2000; 99W0-US03099.
06-JAN-2000; 99W0-US03099.
06-JAN-2000; 2000W0-US00376.
11-FEB-2000; 2000W0-US00376.
11-FEB-2000; 2000W0-US00376.
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2000WO-US023522.
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2000US-0209832P
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2000WO-US030873
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P-PSDB; AAU12408.
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05-JUN-2000; 2
28-JUL-2000; 2
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24-AUG-2000;
08-NOV-2000;
                                                                                              Homo sapiens.
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BP.

AAF44240 standard; cDNA; 713

RESULT 4 AAF44240 (first entry)

02-APR-2001

AAF44240;

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polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptides, and to detect the presence of mammalian lung, colon, creast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in proliferation of inner ear utricular supporting cells or of T-color proliferation of inner ear utricular supporting cells or of T-color proliferation of inner ear utricular supporting cells or of T-color proliferation of inner ear utricular supporting cells or of T-color proliferation of endothelial cells or of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymclecides encoding PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymclecides encoding PRO polypeptides can be used in assays to identify molecules
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Local Similarity 100.0%; Pred. No. 2.7e-155;
Nes 713; Conservative 0; Mismatches 0;
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PJ;
                                                                                      PRO; cytostatic; cell death;
tissue typing;
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Godowski F
Paoni NF;
Wood WI;
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                               (UNQ589) nucleotide sequence SEQ ID NO:376.
                                                                                       protein; mapping;
                                                                                       Human; secreted and transmembrane cancer; chromosomal mapping; gene
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2000WO-US0300376.
2000WO-US03655.
2000WO-US034341.
2000WO-US04414.
2000WO-US04414.
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99US-0144758P.
99US-0145698P.
99US-0146222P.
99US-0149396P.
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2000WO-US005841.
2000WO-US006884.
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99WO-US028313.
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99WO-US030095
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                                                                                                                 diagnostic assay; ss.
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Grimaldi CJ, Gurney
Rov MA, Stewart TA,
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P-PSDB; AAB65271.
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                                                               Human PRO1159
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02-MAR-2000;
15-MAR-2000;
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18-FEB-2000;
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09-JUN-1998;
10-JUN-1998;
                                    Homo sapiens.
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02-JUN-1998;
02-JUN-1998;
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and protein sequence can be used for tissue typing and in treating cancer. Auti-PRO antibodies can be used in diagnostic assays. AAF44270 tAAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF4269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCC
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                                                                                                   Length 713;
                                                                             Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
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                                                                                                   100.0%; Score 713; DB 5; L 100.0%; Pred. No. 2.7e-155;
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liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
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Length 713;

Query Match
100.0%; Score 713; DB 7; Length 7
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels

09 9 TITIGGGATITITAATITICAAACACAGAGAATGACATITITICIGICACTATIATI 120 61 TITIGGGAITITAATITICAAACACAGCAGAATGACATITITICIGTCACTAITAIT 120 121 GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180 CTTTCTATCAAGAAATAAAGAGAACCACAGACCCACACAAATCATCTTAGAAGACAG 240

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TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT 300

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98WO-US019437. 98WO-US021141. 98WO-US021141. 98WO-US021141. 99WO-US000106. 99WO-US000106. 99WO-US012252. 99US-0141037P. 99US-014368P. 99US-0144368P. 99US-0144528P. 99US-0144528P. 99US-0146222P. 99US-0146222P. 99US-0146222P. 99US-0146222P. 99WO-US021090. 99WO-US021199.	0WO - USO 0021 0WO - USO 0035 0WO - USO 0045 0WO - USO 0441 0WO - USO 0491 0WO - USO 0631 0WO - USO 0631 0WO - USO 0633 0WO - USO 1335 0WO - USO 1345 0WO - USO 1352 0WO - USO 1352 0WO - USO 1352 0WO - USO 1353 0WO - USO 1353 0WO - USO 1353 0WO - USO 1353 0WO - USO 1353 0WO - USO 1353 0WO - USO 2352 0WO - USO 2352 0WO - USO 2352
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                                                 GTATCCCTGTCATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC
                                                                     GTATCCCTGTCATATACATAAGGTGAATTATAAGTACCCTATGCAGTTGGCTGGAC
                                                                                                                                                                                           TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATAGAAAGG
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                                                                                                                 AGTICIAAATIGGACITIAITAATITITIAAAATCAGIAACIGATITIATCACIGGCIATGI
                                                                                                                                    GCTTAGATCTACAGGAGATCATATATTTGATACAAATAAAAGAAAAGTGTTCTCCCC
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97US-0062260P.
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12-NOV-1997;
13-NOV-1997;
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DL; Godowski P Paoni NF; Wood WI;

Goddard A, MA, Pan J, Williams PM,

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Novel isolated PRO polypeptides e.g., PROB26, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
                                       Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Ferrara N, Fong S, Gerber H, Gerritsen ME, Godda Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, PROY MA, Stewart TA, Tumas D, Watanabe CK, Willia
                                                                                                                                                           Claim 2; Fig 273; 648pp; English.
        28-AUG-2001; 2001US-00941992.
                        (GETH ) GENENTECH INC.
                                                                                          WPI; 2003-247083/24.
P-PSDB; ABUS9165.
                                                                                                                                            treatments
                                                                         Zhang Z;
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DB 7; Length 713; Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other; represents a novel human PRO protein polynucleotide

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                                                                      AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTTATTCCAATAACATTTGGG
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     100.0%; Score 713; DB 7; L
100.0%; Pred. No. 2.7e-155;
ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
Matches 713; Conservative
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(first entry)

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Human; secreted and transmembrane protein; PRO; antiinflammatory; antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidabetic; gene therapy; tumour necrosis factor (TMF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing; gene; ss.
                                                        Novel human secreted and transmembrane protein PRO1159 cDNA.
                                                                                                                                                                                                                          US2003032156-A1.
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Pred. No. 2.7e-155;
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2000WO-US01564.
2000WS-0213637P.
2000WO-US020710.
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2000WO-US014042
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         24-FEB-2000;
24-FEB-2000;
02-MAR-2000;
10-MAR-2000;
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20-MAR-2000;
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29.NOV-1999;
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RESULT 8 ACD24089 ID ACD24089 standard; CDNA; 713

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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences
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2001WO-US0066220.
2001US-00802706.
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30-MAY-2000;
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28-JUL-2000;
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Gao W;

Sherwood S;

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are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNR)-alpha from human blood, modulate the publisher or fire proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood monounclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The mucleic confidences, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immundofficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful an biarmace typing. This sequence encodes a novel human secreted and transmembrane PRO
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100.0%; Pred. No. 2.7e-155;
iive 0; Mismatches 0;
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Human, gene, ss, PRO, secreted, transmembrane, signal peptide, pharmaceutical, diagnostic, therapeutic, gene therapy.
                                                               Human secreted/transmembrane protein cDNA, #154.
               ABX90341 standard; cDNA; 713 BP.
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970S-006250P.
970S-006511P.
970S-006511P.
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                                              01-MAY-2003 (first entry)
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25-FEB-1998;
20-MAR-1998;
28-APR-1998;
07-MAY-1998;
08-MAY-1998;
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13-NOV-1997
                               ABX90341;
RESULT 9
ABX90341
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06-JAN-2000; 2000W0-US000376.
11-FEB-2000; 2000W0-US000376.
12-FEB-2000; 2000W0-US004414.
24-FEB-2000; 2000W0-US004414.
24-FEB-2000; 2000W0-US004914.
24-FEB-2000; 2000W0-US005114.
24-FEB-2000; 2000W0-US005114.
15-MAR-2000; 2000W0-US005119.
15-MAR-2000; 2000W0-US005119.
15-MAR-2000; 2000W0-US005119.
15-MAY-2000; 2000W0-US008419.
11-MAY-2000; 2000W0-US0113705.
20-MAR-2000; 2000W0-US0113705.
20-MAR-2000; 2000W0-US0113705.
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20-MAR-2000; 2000W0-US0113705.
20-MAR-2000; 2000W0-US0113705.
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23-AUG-2000; 2000WO-US023282.
24-AUG-2000; 2000WO-US03328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FRB-2001; 2001WO-US032678.
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99WO-US030911.
2000WO-US000219.
2000WO-US00376.
2000WO-US003565.
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99WO-US01252.
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99WO-US028313.
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2000WO-US020710.
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(GETH) GENENTECH INC.

. DL; Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton I Perrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, (Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, I Rov MA. Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;

WPI; 2003-288106/28. P-PSDB; ABU60595.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.

Claim 2; Fig 271; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive on bloodstally bind to the PRO polypeptide, for linking a bioactive one biological activity of a cell. The PRO polypeptides or polymucleotides are also useful in gene therapy, in chromosome dentification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated mucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or

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     gene therapy; gene; ss.
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                          Homo sapiens
                                                                                      20-NOV-2001;
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natural sources. The sequences presented in ABX90083-ABX90468 are the genes encooding, the primers amplifying and the probes detecting the PRO polymucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
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                                                                                                                                                                                         TTTTGGGATTTTTAATTTTCAAACAGCAGAATGACATTTTTTCTGTCACTTATTATTATT
                                                                                                                                                                                                                                                        CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTAGAAGACAG
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                                                                                   100.0%; Score 713; DB 7; Length 713; 100.0%; Pred. No. 2.7e-155;
                                                           Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
                                                                                                         Indels
                                                                                                         0; Mismatches
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                                          seqdata.uspto.gov/sequence.html
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Best Local Similarity 100.
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TTTTGGGATTTTTAATTTTTCAAACACAGGAGAATGACATTTTTTTCTGTCACTATTATTATT GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA GTIGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA CTTTCTATCAAGAAATAAAGAAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT

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AATATATCATCTATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG

TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT GTATCCCTGTCATATACAATAAGGTGAATTATAAGTACCCTATGCAGTTGGCTGGAC GTATCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC

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Godowski P. Paoni NF; Wood WI;

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TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT 300

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AGTICTAAATTGGACTTTATTAAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGT AGTTCTAAATTGGACTTTATTAATTTTTTAAATCAGTAACTGATTTATCACTGGCTATGT GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCCCC 900

541 GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCC

TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG

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AAGAATGACAGGGAGAAAGGAAAGAGGGAAAATGTTGCCAAGGAAAAAA 713

ACA67230 standard; cDNA; 713

RESULT 11 ACA67230 ACA67230;

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Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                  2000WO-US004341.
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from the USPTO web site at sec
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22-MAY-2000;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for modulating bioactive molecules to cells expressing PRO polypeptides, for modulating calculations of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therzapy, for chromosome calculation, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. The present sequence encodes a human PRO polypeptide of the invention, one control of an analysis and manalysis and an analysis. this patent was obtained in electronic format directly site at seqdata.uspto.gov/psipsDIDEntry.html Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers. Claim 2; Fig 271; 649pp; English.

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Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; diabetes; bone disorder; cartilage disorder; rheumatoid arthritis; obesity; sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia; hearing loss; coagulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
                                                                                              cDNA encoding human PRO polypeptide #237.
                                                               (first entry)
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Query Match

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The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Active proteins in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. Act66994.Act6768 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this parent was obtained in electronic format directly from the USPTO web
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0;
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11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US004414.

22-FEB-2000; 2000WO-US004114.

24-FEB-2000; 2000WO-US004314.

24-FEB-2000; 2000WO-US005004.
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                                             CTTTCTATCAAGAAATAAAGAGAACCACAGTCAAACCACACAATCATCTTTAGAAGACAG
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                     TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted
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Godowski PJ;
Paoni NF;
Wood WI;
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             2000WO-US015264.
2000WO-US020710.
2000WO-US022031.
2000WO-US023522.
2000WO-US023328.
2000WO-US033958.
                                                                                                    01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
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2001WO-US019692.
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09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.
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Matches 713; Conservative
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     10-MAR-1999;
20-APR-1999;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating bioactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for thuran blood, for stimulating the proliferation or differentiation of month blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with consume and in gene therapy. ACA03603-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
                                                                                                                                                                                                                                                                                                  Gao W;
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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20-JUN-2001; 2001MO-US019692.
22-JUN-2001; 2001WS-00887879.
22-JUN-2001; 2001WO-US021016.
29-JUL-2001; 2001MO-US021066.
09-JUL-2001; 2001MO-US021056.
06-AUG-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
16-AUG-2001; 2001US-00921796.
16-DEC-2001; 2001US-00931836.
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ME, Goddard A,
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Smith V,
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121 GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180

CTTTCTATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG

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241 TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT 300 TGACTCAAGAGGGTTAATTCTTGGTGCTGAAGCCTGGGGGCAGGGGTGTAAAGAAAACAC 360

TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAAGGACGGAATCT

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99WO-US008615.
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                                                                                                                                                                                                                                                        DNA encoding novel secreted and transmembrane protein PRO1159.
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14-SEP-1998;
14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
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07-OCT-1998;
29-OCT-1998;
29-OCT-1998;
20-NOV-1998;
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05-JAN-1999;
08-MAR-1999;
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24-NOV-1997;
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28-APR-1998
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                                                                                                                                                                                                                                                                               Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
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A, Godowski PJ, Gurney AL, Sherwood S;
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            22-JUN-2001; 2001WO-US020116.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2201; 2001WS-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00921796.
16-AUG-2001; 2001US-00931836.
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P-PSDB; ABU59887.
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Database : 'GenEmbl:* 1

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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     Tumas, D., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment
diseases
Patent: WO 0073452-A 82 07-DEC-2000;
Genentech, Inc. (US)
Location/Qualifiers
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      TITIGGGAITITIAATITITCAAACACAGCAGAATGACATITITITICIGTCACTATIATIAT
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llarity 100.0%; Pred. No. 7.3e-136;
Conservative 0; Mismatches 0;
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Location/Qualifiers
1. .713
/organism="unknown"
/mol_type="genomic DNA"
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PAT 14-JUN-2002 713 linear AX403489 7 713 bp 1 Sequence 376 from Patent WO0073454. AX403489 GI:21436980 . Homo sapiens (human) AX403489.1 RESULT 3
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Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J., Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,

LOCUS
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RESULT 2 AX055452

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SOURCE ORGANISM

REFERENCE AUTHORS

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Query Match
100.0%; Score 713; DB 6; L
Best Local Similarity 100.0%; Pred. No. 7.3e-136;
Matches 713; Conservative 0; Mismatches 0;
                             DNA
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Genentech Inc. (US)
Location/Qualifiers

    713
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                           713 bp
WO0140466.
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                                                               AX464340.1 GI:21899186
                                                                                        Homo sapiens (human)
Homo sapiens
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                                   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godwski,P., Grimaldi,C.J., Gurney,A.L., Kijavin,I., Napier,M.A., Pan,J., Walliams,P., Nov,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.L. and Zhang,Z. Secreted and transmembrane polypeptides and nucleic acids encoding Patent: WO 0073454-A. 376 07-DEC-2000; Genentech Inc. (US)
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Catarrhini; Hominidae; Homo.
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Pred. No. 7.3e-136;
0; Mismatches 0;
                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Location/Qualifiers
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PAT 16-JUL-2002 Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding 120 480 900 GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180 GTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACACATTGGAGAATGGCTA 180 240 240 300 300 TGACTCAAGAGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACAC 360 TGACTCAAGAGGTTAATTCTTGGTGCTGAAGCCTTGGGGGCAGGGGTGTAAAGAAAAACAC 360 420 TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT 420 480 540 540 600 099 9 09 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCT TGTGACTCCTACCAAAGCTGTCAAAAACCACAGGGAAGGGCATAGTTAAAGGACGGAATCT AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTTTTCCAATAACATTTGGG CITICIATCAAGAAATAAAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAG **AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGG** GTATCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC GCTTAGATCTACAGGAGATCATATATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCC TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT GTATCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGAC AGTICIAAATIGGACITIAATITITAAAAICAGIAACIGATITAICACIGGCIAIGI AGTICTAAATIGGACTITATIAATITTITAAATCAGTAACTGATTTATCACTGGCTATGT GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCC TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG Gaps 0; Length 713; linear Indels

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                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)

2 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Roster, J., Grimaldi, C., Gu, Q., Hass, P. B., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagirti, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Goddwski, P., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAQ89048.1"
| db_xref="Gg1:37182492"
| translation="MTFFISELLIVCEAIMENSOSGNTLENGYFLSRNKENHSQPTQ
| SSLEDSVTPTKAVKTTGKGIVKGRNLDSRGLILGAEAMGRGVKKNT"
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   601 TTACAGAATTGACATTTTAAATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGG 660
                                                                                                                              Homo sapiens clone DNA60627_CLECSF12 (UNQ589) mRNA, complete cds. AY358685 AY36865.1 GI:37182491
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Direct Submission

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA May, South San Francisco, CA 94080, USA

Location/Qualifiers
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llarity 100.0%; Pred. No. 7.3e-136;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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/note="PR01159"
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CTITICIALIZAGAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACCAG
                                                                                                                                                         TTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAT
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                                   TGTGACTCCTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAAGGACGGAATCT
                                                                                                                                                                                                                                                                                  AGTICTAAATIGGACTITATTAATTITTAAAATCAGTAACTGATTTATCACTGGCTAIGT
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Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marting, R., Martindale, A., Martinez, E., Massey, E., Manniney, E., McLeod, M.P., Medor, M., Marting, E., McLeod, M.P., Medor, M., Maride, Merscher, S., McLeod, M.P., Medor, M., Miller, S., Miller, S., Miller, S., Moser, M., Mohlson, D., Newtson, M., Mortis, S., Moser, M., Newtson, D., Newtson, M., Newtson, M., Newtson, A., Nguyen, N., Nguyen, N., Nickerson, E., Primus, E., Pui, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pui, L.L., Quiles, M., Ren, Y., Riyos, M., Oviedo, R., Pare, M., Rolfe, M., Raiz, S., Savery, G., Scherer, S., Soott, G., Shen, H., Shim, C., Shooshtari, N., Sisson, I., Sutcon, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Stunes, N., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlingson, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Welington, C., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On May 29, 2002 this sequence version replaced gi:21206012.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

gc-help@bcm.tmc.edu

COMMENT

ANNOTATION OF FEATURES:

SISs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base

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'note="Variable size of homopolymeric repeat in subclones"
function="unresolved homopolymeric run"
quality are listed below. Description of the metrics can be found
               at URL:
http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
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6224. .16401
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complement(13288..13579)
/rpt_family="MLTIA1"
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complement(13580. .13891)
/rpc_family="AluJo"
complement(13892. .13987)
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                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/rpt_family="MIR" 3137)
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complement(2987, .3137)
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/rpt_family="Charlie2"
complement(6577 .6703)
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6980. .7102
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/rpt_family="MLT1D"
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6420. .6491
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complement(7215...750)
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complement(9745. .100
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complement(15682..16)
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/rpt_family="THE1B"
18054. .18101
/rpt_family="MIR"
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                                                                                                                                                          clone="RP11-133L14"
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complement (4558. .46
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1859. .4941
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complement(12307...
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19837. 19882
/rpt_family="(TA)n"
complement_20182. 20549)
20550. 21060
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complement(21061. 21138)
/rpt_family="LiMC2"
complement(21141. 21268)
/rpt_family="MER52C"
22220. 22301
/rpt_family="AluJ/FLAM"
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'rpt_family="LIM2"
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211631 TGTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCT 211572
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Mus musculus chromosome UNK clone RP23-250B1, WORKING DRAFT
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Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park
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HTG: HTGS PHASEL; HTGS_ENEPT; HTGS_FULLTOP.
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
HCBASTSON, J. D. and Waterston, R. H.
The sequence of Mus musculus clone
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                                              ACTITIC-TATCAAGAAATAAAGAGAACCACAGT-CAACCCACACAATCATCTTAGAAGA
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On Feb 25, 2003 this sequence version replaced gi:27657609
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Center code: WUGSC
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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    Chemistry: Dye-terminator Big Dye: 23% of reads
Assembly program: Phrap; version 0.990129
Consensus quality: 71594 bases at least Q40
Consensus quality: 71594 bases at least Q40
Consensus quality: 110702 bases at least Q20
Estimated insert size: 229041; sum-of-contigs estimation
Estimated insert size: 2310100; agarose-fp estimation
Quality coverage: 0.6x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
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Pred. No. 3.9e-111;
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// Corganism="Homo sapiens"
// All type="genomic DNA"
// Ab xref="taxon:9606"
// clone="RP11-13C13, RP11-656E20"
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                                                                                                                                                                                                                                                                                                  Insert size: 193000; agarose-fp
Insert size: 227132; sum-of-contigs
Quality coverage: 14.88 in Q20 bases; agarose-fp
Quality coverage: 12.33 in Q20 bases; sum-of-contigs
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171559: gap of unknown length
221471: contig of 49912 bp in length.
                                           Sequencing vector: M3; 0%
Sequencing vector: M3; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-brimer ET; 0% of reads
Assembly program: Phrap; version 0.999319
Consensus quality: 218068 bases at least Q30
Consensus quality: 2189373 bases at least Q30
Consensus quality: 2189373 bases at least Q20
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note="assembly_name:Contig24"
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'note="assembly_name:Contig23"
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note="assembly_name:Contig19"
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note="assembly_name:Contig21"
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/note="assembly_name:Contig25"
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/note="assembly_name:Contig26"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
name: M BA0250E01
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*** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 AGTGTAATGTATCCCTGTCATATATACAATAAGGTGAAATTATAAGTACCCTATGCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86763 - AATATGTTTACATCTACTAACAĞTGAATTCAAĞĞCAAĞÇAĞÇÇÇAACAĞAATTÇÇÇTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86704 AGCATAACATA-ÇCCTGCCAGACAGCTGGTAAAGTGGCATCACAAATCCACAGCTĆ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTATGTGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAAGAAAAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ATTGTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACTTGGAGAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86992 GTTCGTGACGTATGAAGCATTTTTGGTGACACAATTCAGGGAGAAATCCAGAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86932 CAACTICCTAICAAGAAATAAAGAGAACCACA--AGCCCACAGAAICATCTITAGAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 CAGIGIGACICCIACCAAAGCIGICAAAACCACAGGCAAAGGGCAIAGIIAAAAGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 AAAAACACTTAGATTCAATGATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTTGGGGATTTTTAATTTTCAAACACAGCAGAATGACAT--TTTTTCTGTCACTATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACTTTCTATCAAGAAATAAAGAGAACCACACACCACACAATCATCTTTAGAAGA
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                                                                                                                                                                                                                                                                                                   51;
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                                                                                                                                                                                                                                                   Length 221471;
                                                                                                                                                                                                                                                      26.1%; Score 186; DB 2; Length 22 63.2%; Pred. No. 1.7e-28; rative 0; Mismatches 215; Indels
/note="assembly_name:Contig28"
80993. .103312
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126015. .171459
/note="assembly_name:Contig31"
171560. .221471
/note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC112033 273867 bp D
Rattus norvegicus clone CH230-94G2,
2 unordered pieces.
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2 ATATATCATCTATTTATCATTAATCAATAATGTATTCT-TTTATTCCAATAACATTTGGG 60
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10 (Dases I to 273867)

11 (Dases I to 273867)

12 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anguale, Merzker, M. Lee., Abramzon, S., Addams, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anguale, D., Anguale, A., Ayodeji, M., Bacale, E., Badan, H., Baldan, D., Bandaranake, D., Barber, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Barnstead, M., Carter, M., Chardson, C., Cavalean, T., Censar, M., Charnstead, M., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., Chan, S., McLeed, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., M
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                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                          AC112033.3 GI:23667218
HTG, HTGS PHASE1, HTGS_DRAFT, HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Rat Genome Sequencing Consortium.
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Worley, K.C.
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consists entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center close name: CH230-94G2

Assembly program: Phrap; version 0.990329

Consensus quality: 244419 bases at least Q40

Consensus quality: 244702 bases at least Q30

Consensus quality: 247044 bases at least Q30

Consensus quality: 247002 bases at least Q20

Estimated insert size: 254595; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Best Local Similarity 71.7%; Pred. No. 1.2e-20;
Matches 251; Conservative 0; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .273867
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
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clone_end:T7"
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/note="clone_boundary
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/note="clone_boundary
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clone_end:T7
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L. .1354
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Qeikrtyvnphnhl"
                                                                                                                                                                                                                                                              16206 AGGIGGCTCCCCCCAAGCCATCCCAAACTACAGGCAAAGGGCAGAACTAAAGGAGCAATGG 46265
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens beta-glucan receptor isoform H (BGR) mRNA, complete cds, alternatively spliced.
AF400602.
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                   46028
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1 (bases 1 to 881)
Willment, J.A., Gordon, S. and Brown, G.D.
Gharacterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
                                                                                                                                   46089 CGCGCATATGAAGCATTTCGCAGATTCAATTTCAGGGAGATATCCAGAGAGAAAGACA
180 ACTITICIATICAAGAAATAAAGAGAACCACACAGTCAACCACACAATCATCTTTAGAAGACA
                                                                                                                                                                                                  46149 ACTICCCAICAAGAAATAAGGAGAACCACA--AACCCACAGAACCAICTITAGAIGAGA
                                                TITITGGGATITITAATITICAAACACAGCAGAATGACAIT-TITICTGTCACTATTATTAT
                                                                        TGTTGGTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACTTGGAGAATGGCT
                                                                                                                                                                                                                                    240 GTGTGACTCCTACCAAAGCTGTCAAAACCACAGGCCAAGGGCATAGTTAAAGGA----CG
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3RE, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..351
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/note="C-type lectin BGRH; alternatively spliced"
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/br.ete="GI:15986714".
                                                                                                                                                                                                                                                                                                                             46266 GATCCTGGATTCCAGAGGTTCATTTCCTGGTACTGAGGCTTGGGGTGGGG 46315
                                                                                                                                                                                                                                                                                                  344
                                                                                                                                                                                                                                                                                                  GAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 881)
Willment, J.A., Gordon, S. and Brown, G.D.
Direct Submission
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mol_type="mRNA"
/mol_type="mRNA"
/db.xref="taxon:9606"
/chromosome="12"
/map="12p13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="BGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                        15969
                                                     61
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TITLE
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AF400602
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MEDLINE
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KEYWORDS
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Gaps

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Indels

19.9%; Score 142; DB 9; L 100.0%; Pred. No. 3.9e-19; iive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 142; Conservative

Length 881;

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SVRETLSDQNHSYPRKPISKLCMDSRVSHL"
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mRNA, complete
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1; alternatively spliced"
                                        309
                                                                                   251
                                                                                                            191
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 BATABAGAGAACCACAGTGAACCCACAATCATCTTTAGAAGACAGTGTGACTCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 GCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 GCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGA
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                                    250 AAGCTATTTGGAGATCCAATTCAGGAAGCAACAACACATTGGAGAATGGCTACTTTCTATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
132 AAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAA
                                                                                 GAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pathology,
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Willment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its
alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
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Willment, J.A., Gordon, S. and Brown, G.D.
Direct Submission
Submitted (18-JUJ-2001) Sir William Dunn School of Pa
Oxford University, South Parks Road, Oxford OX1 3RE,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 625;
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                                                                                                                                                                                                                                                                                                   625 bp mRNA linear
Homo sapiens beta-glucan receptor isoform C (BGR)
cds, alternatively spliced.
AF400597
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Pred. No. 1e-18;
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sal Similarity 100.0%; Pred. No. 1e-
140; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                              CCAAAGCTGTCAAAACCACAGG 273
                                                                                                                                                                                                    370 CCAAAGCTGTCAAAACCACAGG 391
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Matches 140
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 744)
Herman2-Falcon, P., Arce, I., Roda-Navarro, P. and Fernandez-Ruiz, E.
Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene expressed on dendritic cells
Immunogenetics 53 (4), 288-295 (2001)
11491532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="MEYHPDI-BNLDEDGYTQLHFDSQSNTR1AVVSEKGSCAASPPWR
L1AVILGILCLVILVIAVVLGTMAIWRSNGSSNTLENGYFLSRNKENHSQFTQSSLED
SYPTFARAVETGYLSRECPPWIITENSECYLFSMSLNSWDGSKRQCWQLGSNLIKIDS
SNELGFIVKQVSSQFDNSFWTGLSRECYEVWIMEDGSTFSSNLFQIRTTATQENPSP
NCVWIHVSVIYDQLCSVPSYSICEKKFSM"
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Homo sapiens lectin-like receptor 1 (DECTIN1) mRNA, complete cds.
AY026769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="C-type lectin BGRA; similar to Mus musculus dectin
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                                                                                                                                                                                                                                       Direct Submission

Willment, J.A., Gordon, S. and Brown, G.D.

Direct Submission

Submitted (18-JU-2001) Sir William Dunn School of Pathology,

Oxford University, South Parks Road, Oxford OX1 3RE, UK

Location/Qualifiers
(bases 1 to 74)
Willment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
11567029
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1. .744
/gene="BGR"
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| product== beta=11711.1"
| protet=in_id="AAL11711.1"
| db_xref="GI:15986700"
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Pred. No. 1e-18;
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100.0%; Pred. No. 10. 10. 0; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/map="12p13"
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/gene="BGR"
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Homo sapiens
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Best Local Similarity
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ACCESSION
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ORGANISM
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AUTHORS
TITLE
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PUBMED
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AY026769
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Homo sapiens beta-glucan receptor isoform A (BGR) mRNA, complete
AF400595
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PN JP 1999001497-A/2
PN OF JAN-1999
PF 13-JUN-1999
PF 13-JUN-1997
PE SHUJI HINUMA, SHOJI FUKUZUMI, KAZUNORI NISHI, YASUSHI ARAYA PC CO7K14/47, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (C12N1/21,C12R1:19), (C12N15/09,C12R1:91),A61K37/02,A61K37/02,
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| Jorganism='Unidentified'.
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                                                                                                                                                                                                                                                                                                                                                                            unidentified
unclassified.
(Dases 1 to 741)
Shuji,H., Shoji,F., Kazunori,N. and Yasushi,A.
Novel membrane protein and DNA thereof
Patent: JP 1999001497-A 2 06-JAN-1999;
TAKEDA CHEM IND LED
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Pred. No. 1e-18;
                                                                                                                                                                                                                      E21012
Novel membrane protein and DNA thereof.
E21012
E21012.1 GI:13023572
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    .741
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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                                                                         322 AAAGCTGTCAAAACCACAGG 341
                                              254 AAAGCTGTCAAAACCACAGG 273
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ilarity 100.0%; Pr
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Homo sapiens
                                                                                                                                                                                                                                                                                                                              JP 1999001497-A/2. unidentified
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ncvwiihvsviydQlcsvpsysicekkesm"
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1 (bases 1 to 787)
Willment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
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      2 (bases 1 to 744)
3 Herranz-Falloon, P., Arce, I. and Fernandez-Ruiz, E.
Direct Submission
Commission
Submitted (01-FEB-2001) Biologia Molecular, Hospital de la princesa, Diego de Leon 62, Madrid 28006, Spain
E. 3 (bases 1 to 744)
S Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.
Direct Submission
Committed (05-007-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain
Sequence update by submitter
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protein_id="AAK20114.2"
db_xref="G1:15967097"
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Willment, J.A., Gordon, S. and Brown, G.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/gene="DECTIN1"
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Homo sapiens
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Stewart, Timothy A.
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Botstein, David
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Grimaldi, J. Christopher
Gurney, Austin L.
                               Gerber, Hanspeter
Gerritsen, Mary E.
                                                                           Godowski, Paul J.
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                                                            Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botestein, pavid
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Best Local Similarity:
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A APPLICATION NUMBER: 60/089653

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                 332 GCCTGGGGCAGGGTGTAAAGAAAACACT 361
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PRIOR PILING DATE: 1998-0-6-0

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PRIOR PILING DATE: 1998-0-6-03

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                                                                                                                          Coll 999-279-376
Sequence 376, Application US/09989279
Patent No. US20020072496A1
GENERAL INFRMATION:
APPLICANT: Ashkenazi, Avi J.
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Grimaldi, J. Christopher
Gurney, Austin L.
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Watanabe, Colin K.
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Napier,Mary A.
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Patent No. US20020072497A1
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APPLICANT: Ashkenazi, Avi J.
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Matches:
Conservative:
Mismatches:
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FILING DATE: 1998-07-09
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ATTLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC65

CURRENT APPLICATION NUMBER: US/09/989,727

CURRENT APPLICATION NUMBER: 60/06220

PRIOR APPLICATION NUMBER: 60/06220

PRIOR PILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06210

PRIOR PILING DATE: 1997-11-12

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PRIOR PILING DATE: 1997-11-24

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US-09-989-293A-377 (1-90) x US-09-989-279-376 (1-713)

Indels:

Percent Similarity: Best Local Similarity: Query Match:

3.38e-57 462.00 100.00% 100.00%

Pred. No.:

1998-06-00 NUMBER: 60, 1998-06-00 NUMBER: 60, 1998-06-00 NUMBER: 60, 1998-06-00 NUMBER: 60, 1998-06-00 NUMBER: 60, 1998-06-00 NUMBER: 60, 1998-06-00 NUMBER: 60, NUMBER: 60, NUMBER: 60, NUMBER: 60, NUMBER: 60, NUMBER: 60,	1998-06-06 NUMBER: 600 NUMBER: 600 NUMBER: 600 1998-06-06 NUMBER: 600 1998-06-06 NUMBER: 600	
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CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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Patent No. US20020103125A1
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Gurney, Austin L.
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Napier, Mary A.
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Botstein, David
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                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                              Alignment Scores:
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R APPLICATION NUMBER: 60/088926
R RAPLICATION NUMBER: 60/088926
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08858
R APPLICATION NUMBER: 60/088661
R APPLICATION NUMBER: 60/088661
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R APPLICATION NUMBER: 60/088734
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R APPLICATION NUMBER: 60/088738
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R APPLICATION NUMBER: 60/088742
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NR APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-05-07

NR FILING DATE: 1998-05-07

NR FILING DATE: 1998-05-08

NR APPLICATION NUMBER: 60/087607

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R APPLICATION NUMBER: 60/086212
R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/08955
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A APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/078910
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212 CAACCCACACAATCATCTTTAGAAGACAGTGTGGACTCCTACCAAAGCTGTCAAAACCACA 271 272 GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331 152 TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT 211 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80 92 ATGACATITITITCTGTCACTATTATTATTATTGTTGGTATGTGAGAGCTATTTGGAGATCCAAT 1 MetThrPhePheLeuSerLeuLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 7113 90 0 0 0 0 Conservative: Mismatches: Indels: US-09-989-293A-377 (1-90) x US-09-989-731-376 (1-713) Length: Matches: 332 geergegeckégégrérkkákákákákáckér 361 AlarrpGlyArgGlyValLysLysAsnThr 90 R FILING DATE: 1998-07-02

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R APPLICATION NUMBER: 60/091633

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091633

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/09198

R FILING DATE: 1998-07-07

R APPLICATION NUMBER: 60/091982

R FILING DATE: 1998-07-07

R APPLICATION NUMBER: 60/091982

R FILING DATE: 1998-07-07 Sequence 376, Application US/09989732 Patent No. US20020123463A1 Grimaldi, J. Christopher Gurney, Austin L. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey 3.38e-57 462.00 100.00% 100.00% Eaton, Dan L. Ferrara, Napoleone Gerritsen, Mary E. Paoni, Nicholas F. Godowski, Paul J Kljavin, Ivar J. Napier, Mary A. GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. Baker, Kevin P. Botstein, David Goddard, Audrey Desnoyers, Luc Fong, Sherman Рап, Јашев Percent Similarity: Best Local Similarity: -09-989-732-376 Alignment Scores: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 6/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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              APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                        FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                              PRIOR PELICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065111
PRIOR APPLICATION NUMBER: 60/065111
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1997-11-24
PRIOR PLING DATE: 1998-102-25
PRIOR PRIOR DATE: 1998-102-25
PRIOR PLING DATE: 1998-102-25
PRIOR PLING DATE: 1998-102-25
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-07
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PRIOR PLING DATE: 1998-06-07
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PRIOR PRING DATE: 1998-06-10
PRIOR PRING DATE: 1998-06-07
PRIOR PRING DATE: 1998-06-07
PR
           Wood, William I.
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APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR REPERGENCE: P. 2011-11-14
PRIOR APPLICATION NUMBER: 05/049787
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PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/08803
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                                                                                            Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                           Timothy A
                                                                                                                                                                                                Napier, Mary A.
Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                Roy, Margaret Ann
                                                                     Godowski, Paul J.
                                                                                                                                                               Kljavin, Ivar J.
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Stewart, ....
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Sequence 376, Application US/09991073
Fatent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Beter,Kevin P.
APPLICANT: Beter,Kevin P.
APPLICANT: Beter, Avi J.
APPLICANT: Beton,David
APPLICANT: Feron,Vanid
APPLICANT: Feron,Vanid
APPLICANT: Feron,Application
APPLICANT: Fong,Abreman
APPLICANT: Gerber,Hanspeter
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-66-25
PRIOR FILING DATE: 1998-66-25
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PRIOR FILING DATE: 1998-06-26
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212 CAACCCACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTGAAACCAA 271 272 GGCAAQGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331 92 AIGACAITITITCIGICACIAITAITAITGIIGGIAIGIGAAGCIAITIGGAGAICCAAI 151 152 rcaggaagcaacarruggagaarggcracrircrarcaagaaraagagaaccacagr 211 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer Matches: Conservative: Mismatches: Indels: US-09-989-293A-377 (1-90) x US-09-991-073-376 (1-713) AlaTrpGlyArgGlyValLysLysAsnThr 90 ength: NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090557

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NR FILING DATE: 1998-06-26

NR APPLICATION NUMBER: 60/091408

NR FILING DATE: 1998-07-01

NR APPLICATION NUMBER: 60/091448

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NR FILING DATE: 1998-07-01 R FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09 3.38e-57 462.00 100.00% 100.00% FILING DATE: 1998-07-02 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 21 81 41 61 PRIOR
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APPLICATION WUMBER: 60/090254
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089907
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P730PIGS
CURRENT FILING DATE: 2001.1-14
PRIOR APPLICATION NUMBER: 60/06256
PRIOR APPLICATION NUMBER: 60/062186
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLING DATE: 1997-10-12
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PRIOR PLING DATE: 1998-04-25
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                                                                         Sequence 376, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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                                                                     GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr
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Grimaldi, J.Christopher
Gurney, Austin L.
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Eaton, Dan L.
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Matches:
                    PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-24
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FILING DATE: 1998-07-09
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Query Match:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT RILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/04250
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBERS: 60/081759
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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APPLICATION UNDHER: 60/088826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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APPLICATION UNMBER: 60/088033
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/08861
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                         FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087609
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                                                                   FILING DATE: 1998-03-20
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FILING DATE: 1998-06-03
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CURRENT FILING DATE: 2001-11-14

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PILING DATE: 1997-11-12

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Mismatches:
Indels:
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Sequence 376, Application US/09993604
Patent No. US20020137075A1
PAPERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Napier, Mary A.
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Botstein, David
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Eaton, Dan L.
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                                     Percent Similarity:
Best Local Similarity:
Query Match:
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       Pred. No.:
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PRIOR PELICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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PRIOR PELING DATE: 1998-06-19
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 67/091544
FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091519 PRIOR FILING DATE: 1998-07-02 PRIOR APPLICATION WUMBER: 60/091626 PRIOR PLILNG DATE: 1998-07-02 PRIOR APPLICATION WUMBER: 60/091633 PRIOR APPLICATION NUMBER: 60/091633 PRIOR APPLICATION NUMBER: 60/091978 PRIOR APPLICATION NUMBER: 60/091978 PRIOR APPLICATION NUMBER: 60/091962 PRIOR FILING DATE: 1998-07-07 PRIOR FILING DATE: 1998-07-07 PRIOR FILING DATE: 1998-07-07 PRIOR FILING DATE: 1998-07-07	<pre>nment Scores: 3.38e-57</pre>	-989-293A-377 (1-90) x US-09-993-604-376 (1-713)	1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlalleTrpArgSerAsn 20 	21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40	41 GInProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaVallysThrThr 60	61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80 	81 AlaTrpGlyArgGlyVallysLysAsnThr 90 	SULT 11 -09-990-456-376 Sequence 376, Application US/0990456 Sequence 376, Application US/0990456 GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Betsein, David APPLICANT: Betsein, David APPLICANT: Perrara, Napoleone APPLICANT: Pong, Sherman APPLICANT: Pong, Sherman APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Austin L. APPLICANT: Godowski, Paul J. APPLICANT: Granaldi, J. Christopher APPLICANT: Granaldi, J. Christopher APPLICANT: Granaldi, J. Christopher APPLICANT: Granaldi, J. Christopher APPLICANT: Mijames APPLICANT: Napier, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: And Secreted and Transmembrane Polypeptides and Nucleic
PRH PRH PRH PRH PRH PRH PRH PRH PRH PRH	Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB:	-60-SD	YQ da	y da	ko qa	y du	çy qq	RESULT Second Second Second Second APP APP APP APP APP APP APP APP APP AP

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TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
                                                                                                      PRIOR PILLING DATE: 1997-66-16

PRIOR FILLING DATE: 1997-10-17

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APPLICATION NUMBER: 60/088861
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-10
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C55
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PRIOR APPLICATION NUMBER: 06/049787
PRIOR PLILING DATE: 1997-06-16
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PRIOR PRILING DATE: 1998-02-25
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Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
                                                                                                                                                          Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                     Williams, P. Mickey
Wood, William I.
Zhang, Zemin
                                                                                                                                                                                                                                                          Tumas, Daniel
Watanabe, Colin K.
                                                                                                     Napier, Mary A.
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R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
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R APPLICATION NUMBER: 60/092182
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Patent No. US/020142961A1
GENERAL INFORMATION:
APPLICANT: Baker, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                     APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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APPLICATION WUMBER: 60/091626
ALLING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
   APPLICATION NUMBER: 60/090695
FILING DATE: 1938-06-25
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APPLICATION NUMBER: 60/090863
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Eaton, Dan L.
                                                                                                                                APPLICATION NUMBER:
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152 TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT 211 212 CAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTCAAAACCACA 271 272 GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331 92 ATGACATTTTTTCTGTCACTATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAT 151 61 GlyLysGlylleVallysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80 1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 7113 90 0 0 0 Length:
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Conservative:
Mismatches:
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RESULT 13 US-09-992-598-376

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STILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/090355
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APPLICANT: SLANG, ZENING, ZENING, MILLIAM 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: 60/049707

PRIOR FILING DATE: 1997-66-16

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Sequence 376, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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                                                                            APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
                                                                                                            Baker, Kevin P.
Botstein, David
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Eaton, Dan L.
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272 GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331
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                                                                                                      61 GlyLysGlylleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr
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CURRENT FILING DATE: 1907-06-16
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Gurney,Austin L.
Kljavin,Ivar J.
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Fong, Sherman
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Eaton, Dan L.
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APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090355 1998-07-02 1998-07-07 FILING DATE: 1998-06-26 FILING DATE: 1998-06-25 1998-06-19 1998-06-19 FILING DATE: FILING DATE: PRIOR 713 90 0

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FILING DATE: 1998-06-05
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APPLICATION UNDHER: 60/08858
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APPLICATION NUMBER: 60/089532
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: William I.
APPLICANT: Shang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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ITILE OF INVENTION NUMBER: 00/049787
PRIOR PRICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06511
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PRIOR APPLICATION NUMBER: 60/06511
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/075945
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APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
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Grimaldi, J. Christopher
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
     Best Local Similarity: 100.00%
Query Match: 100.00%
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Napier, Mary A.
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US-09-989-735-376
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                                Query Match:
DB:
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Run on:

Sequence:

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Sequence 1. Application US/08772440

Patent No. 6046158

GENERAL INFORMATION:
APPLICANT: Ratizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
INUMBER OF SEQUENCE: 42
CORRESPONDENCE ADDRES:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                           Sequence 7, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 21, Appl
                                                                       Sequence 767, App
Sequence 109, App
                                                                                                                                                                                                                                                                                                                      Sequence 4832, Ap
Sequence 994, App
                                                          Sequence 16544, A
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Sequence 1, Appli
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Sequence 29, Appl
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Sequence 3, Appl
Sequence 1, Appl
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Sequence 101,
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                                                                                                                                             Sequence 18
Sequence 3,
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                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILLING DATE: CONCURRENTLY HEREMITH
CLASSIFICATION: 435
US-09-252-991A-15961

US-09-621-976-3007

US-09-124-000C-2940

US-09-134-001C-767

US-09-134-001C-767

US-09-148-545-109

US-09-148-545-109

US-09-060-488-1

US-09-060-488-1

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US-09-076-594-183

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US-09-762-724-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
   TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: US
ZIP: 77210
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 243, App
Sequence 183, App
Sequence 1899, Ap
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
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Sequence 7, Appli
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561.186 Million cell updates/sec
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Sequence 3,
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-772-440-7
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US-09-107-532A-1899
US-09-908-855-35
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                                                                                                                                                                                                                                                                                                                                                                            682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                 US-09-989-293A-377
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seq length: 200000000
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Match Length
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Database :

Result No.

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COTHER INFORMATION: /note= "clone O40 ovule-specific gene of THER INFORMATION: encoding a cytochrome P450 monooxygenase cother INFORMATION: from pollen tubes of Phalaenopsis" US-08-560-398-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-560-398-3/c
; Sequence 3, Application US/08560398
; Patent No. 597082
; GENERAL INFORMATION:
; APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
APPLICANT: Saguence: 1
APPLICANT: Saguence: 1
APPLICANT: Sighth Floor
; CITY: San Francisco
; STATE: California
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COUNTRY: USA
ZIP: 94111-3834
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIAL
COMPUTER: IBM PC COMPALIAL
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,398
FILING DATE: 17-NOV-1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: BASTIAN KEVIN L.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
RELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                        US-09-989-293A-377 (1-90) x US-08-772-440-7 (1-528)
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75.56%
62.22%
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                    Percent Similarity:
Best Local Similarity:
                                          Alignment Scores:
JS-08-772-440-7
                                                                                                                                            Query Match:
DB:
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APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 GCATITIGGCGACCACAATICAGGGAGAAATCCAGAGGAAAAGACAACTICCTATCAAGA 349
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: $12/444-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TEMPORATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 AAGGCATCCCAAACTACAGGA 427
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; Sequence 7, Application US/08772440
Patent No. 6046158
; GENERAL INFORMATION:
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143.50
74.47%
61.70%
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
    2298 base pairs
                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                    Score:
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (2269)
OTHER INFORMATION: n
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NAME/KEY: SITE
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                                                                                                                                                                                                                                 1567 regalectregaleaceacacaracealagearrerrerrerreredagacarerrage 1508
                                                                                                                                                                                                                                                                                                                                                                                           1447 GCCAACCAAAGATGAACTGCGAATGCCATGCTTTTGCCAGGGCAAACTCTTTACCG 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGluAlaTrpGly 83
                                                                                                                                                                                            19 SerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsn 38
                                                                                                                                                                                                                                                                                                                                                      --ThrProThrLysAlaValLysThrThrGlyLysGlyIleVal---
            1799
24
11
31
15
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                                 Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
                                                                                                                    Gaps:
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EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
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EARLIER FILING DATE: 1997-06-06
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Patent No. 6525174
GENERAL INFORMATION:
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                8.66
70.50
43.21%
29.63%
15.26%
                                                                          Best Local Similarity:
Query Match:
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                                                       Percent Similarity:
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Alignment Scores:
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EARLIER APPLICATION NUMBER: 60/048,900
EARLIER PILING DATE: 1997-06-06
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (2267)
OTHER INFORMATION: n equals a,t,g,
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280 CAIGAAAACCAAAACAAAACTICIAITITCCCAAAICAGCACCACCCTCCCTCCCTCCACGACG 339
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                                                                                        EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
                                             APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
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                     1997-06-0
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SEQ ID NO 183
LENGTH: 2276
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15.04%
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Best Local Similarity:
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Patent No. 6525174

GENERAL INFORMATION:
TILE REPERENCE: POO'PTI
CURRENT FILING DATE: 1998-12-04

CURRENT FILING DATE: 1998-12-04

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: POT'US98/11422

EARLIER PELICATION NUMBER: POT'US98/11422

EARLIER PELICATION NUMBER: 60/049,885

EARLIER FILING DATE: 1997-06-06

EARLIER PELICATION NUMBER: 60/049,375

EARLIER PELICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,881

EARLIER APPLICATION NUMBER: 60/049,886

EARLIER APPLICATION NUMBER: 60/048,886

EARLIER APPLICATION NUMBER: 60/048,886

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

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EARLIER APPLICATION NUMBER: 60/048,896
Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: 60/048,901
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER PELICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,901
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APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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69.50
53.03%
31.82%
15.04%
                                                                                     Best Local Similarity:
Query Match:
                                                      Percent Similarity:
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EARLIER
      Pred. No.:
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Conservative: Mismatches: Length: Matches:

Indels:

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WESULA 1902-142-690A-35

y Sequence 35, Application US/09242690A

p Patent No. 6284534

GENERAL INFORMATION:
APPLICANT: KONDO, KELJI

TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
TITLE OF INVENTION: SAME
FILE REFERENCE: 049441/0118

CURRENT FILING DATE: 1999-02-23

PRIOR PLING DATE: 1997-08-22

PRIOR PLING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: PCT/JP97/02924

PRIOR PLING DATE: 1996-08-23

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 35

LENGTH: 804
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                                       218 cracigioscricacristrosascrircaaasaascacaarirccricarcriroassacc 277
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                                                                                          --AlaValLysThrTh
                                                                                                                            347 ACAGCAAAACCTGCTGTCAATAAAGGAATAACGGATGAAATCTTGAATAATTGTTGTAAT
                 LeuGluAspSerValThrProThrLy
                                                                                                                                                                                           287 TGGTGAAAAGTCTTACATGGGAGAAACTTAAATCTACTGAACGTTTTTTTA 236
                                                                                                                                                                 60 rGlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeu
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Matches:
Conservative:
Mismatches:
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67.00
43.02%
32.56%
14.50%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)..(801)
US-09-242-690A-35
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Best Local Similarity:
Query Match:
DB:
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US-09-908-855-35
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                                                     RESULT 6
US-09-107-532A-1899/c
US-09-107-532A-1899, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: NUCLEIC ACID SABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsn-ThrLeuGl 27
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117
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-989-293A-377 (1-90) x US-09-107-532A-1899 (1-849)
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...649
SEQUENCE DESCRIPTION: SEQ ID NO: 1899:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
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                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                          STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1899:
SEQUENCE CHARACTERISTICS:
340 AGTACCAAGAAAAGTGGA 357
                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSerSer 46
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28
9
              MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,128
FILING DATE: 25-JAN-1996
FILING APPLICATION DATA:
APPLICATION DATE: 25-JAN-1996
FILING DATE: 25-MAY-1995
FILING DATE: 26-APR-1995
FILING DATE: 26-APR-1995
FILING DATE: 26-CT-1994
FILING DATE: 26-CT-1994
FILING DATE: 26-MAY-1994
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 2330 base pairs
nucleic acid
EDNESS: double
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32.56*
14.50*
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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1259.,2059
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
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Pred. No.:
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US-08-557-128-3
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APPLICANT: KAJIWARA, Susumu
APPLICANT: KAJIWARA, Susumu
TITLE OF INVENTION: TRANSFORMATION SYSTEMS FOR THE YEAST
TITLE OF INVENTION: CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
TITLE OF INVENTION: THEREWITH
              GENERAL INCORMATION:
APPLICANT: KONDO, KEIJI
APPLICANT: MURA, YUTAKA
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
FILE REFRENCE: 04941/0118
CURRENT APPLICATION NUMBER: US/09/908,855
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/242,690
PRIOR PELING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: JP 8/241062
PRIOR APPLICATION NUMBER: JP 8/241062
NUMBER OF SEQ ID NOS: 66
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 TTGCGCAATGGGCAGATATC-ACCAACGCCCACGGTGTCACCGGTGCAGGTATCGTCAAG
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Matches:
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Mismatches:
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Candida utilis
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US-09-908-855-35
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Best Local Similarity:
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NAME/KEY: CDS
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STATE: D
COUNTRY:
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LENGTH: 804
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LENGTH: 2330
TYPE: DNA
ORGANISM: Candida utilis
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Query Match:
DB:
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US-09-252-991A-16320
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US-09-908-855-34
; Sequence 34, Application US/09908855
; Patent No. 6610514
; GENERAL INFORMATION:
; APPLICANT: KONDO, KELJI
; APPLICANT: MURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; TITLE OF INVENTION: SAME
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT FILING DATE: 2001-07-20
; PRIOR PLICATION NUMBER: 09/242,690
; PRIOR PLICATION NUMBER: 09/242,690
; PRIOR PLICATION NUMBER: JP 8/241062
; RIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 34
                                                              GENERAL INFORMATION:

APPLICANT: MUDO, KEIJI

APPLICANT: KONDO, KEIJI

APPLICANT: KONDO, KEIJI

TITLE OF INVENTION: SAME

FILE REPERENCE: 049441/0118

CURRENT APPLICATION NUMBER: 1999-02-23

PRIOR FILING DATE: 1997-08-23

PRIOR FILING DATE: 1996-08-23

PRIOR FILING DATE: 1996-08-23

PRIOR FILING DATE: 1996-08-23

PRIOR FILING DATE: 1996-08-23

PRIOR FILING DATE: 1996-08-23

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PALENTIN VOIL 3330

LENGTH: 2330
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Mismatches:
Indels:
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Matches:
                    US-09-242-690A-34; Sequence 34, Application US/09242690A; Patent No. 6284534
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CORGANISM: Candida utilis
US-09-242-690A-34
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Best Local Similarity:
Query Match:
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Sequence 1620.7

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Sequence 1620.7

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16320

LENGTH: 1065
                                                                                                                                                                                                                      1476 CTACTGTGGCTCCACTCTTGGAGCTTTCAAAGAGCACAATTTCCTCATTTGAGGACC 1535
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Mismatches:
Indels:
                                          Conservative:
                                                                                                                                              US-09-989-293A-377 (1-90) x US-09-908-855-34 (1-2330)
                                                           Mismatches:
Indels:
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Matches:
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Sequence 2940, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: LYAND DOUGETEE-Stamm et al

APPLICANT: LYAND SOUGETEE ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUG FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

NUMBER OF SEQ ID NOS: 6812

SOSTWARE: PATENTH VERSION 3.1
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613 ATGGATCTCGAATTATTTGAAGTGAAAGAACGACTATTGCACGTTCCGATGGTAGTGTA 672
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Matches:
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                          TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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US-09-621-976-3007
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US-09-134-000C-2940
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US-09-252-91A-15961/C
US-09-252-91A-15961/C
Sequence 15961, Application US/0925291A
Fatent No. 6551795
GENERAL INFORMATION:
FATELE OF INVENTION:
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FILE REPREBENCE:
FURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR PELICATION NUMBER: US 60/074,190
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1332
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Sequence 3007, Application US/09621976

Patent No. 663963

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

TILE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENERT 0.054Pt2.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 3007
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Ygapop 10.0
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Database

Result No.

2 2 4 5 9 7 8

92 ATGACATTTTTTCTGTCACTATTATTATTGTTAGGTATGTGAAGCTATTTGGAGATCCAAT 151

a

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1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20

US-09-989-293A-377 (1-90) x AAC91481 (1-712)

40

9

80

a

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Claim 48; Fig 41; 218pp; English.
                   99WO-US028565.
99US-0170262P.
99WO-US030911.
                                                                                                           03-MAR-2000; 2000US-0187202P
15-MAR-2000; 2000WO-US006B84,
20-MAR-2000; 2000WO-US07377,
30-MAR-2000; 2000WO-US007537,
30-MAR-2000; 2000WO-US007539,
                                        2000WO-US000219.
     99WO-US028634
99WO-US028551
                                                      2000WO-US003565
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2000WO-US005601
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                                                              2000WO-US004341
                                                                    2000WO-US004342
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                                                                                   2000WO-US004914
                                                                                                                                                                                 Ashkenazi AJ, Baker KI
Gurney AL, Hebert C,
Watanabe CK, Wood WI;
                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                        and diabetes mellitus.
                                                                                                                                                                                                             WPI; 2001-025253/03.
P-PSDB; AAB50922.
                  02-DEC-1999;
09-DEC-1999;
20-DEC-1999;
05-JAN-2000; 2
                                                     11.F3B.2000; 2
18.FEB.2000; 2
18.FEB.2000; 2
24.FEB.2000; 2
44.FEB.2000; 2
14.FEB.2000; 2
02.MAR.2000; 2
                                                                                                                                                 17-MAY-2000;
     01-DEC-1999;
02-DEC-1999;
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The present sequence is one of thirty three nucleic acids encoding PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antipognists are useful for treating and diagnosing immune related actions such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, didopathic inflammatory myopathies, Signen's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, didopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary bilary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's skin diseases such as asthma, allergic rhinitis, atopic dermatitis, skin diseases such as asthma, allergic rhinitis, atopic dermatitis, cod hypersensitivity and urticaria, idiopathic pulmonary fibrosis and inclusing contact sensitivity in as each of immunely associated diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and inclusing contact sensitivity and urticaria, idiopated diseases such as asthma, allergic pulmonary fibrosis and chinical as collaborates.
                                                                                                                                                                                                                                                                                           Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis
                                                Tumas D;
        Godowski PJ;
Shelton DL,
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Conservative:
Mismatches:
Indels:
Baker KP, Chan B, Goddard A,
bert C, Henzel W, Kabakoff RC,
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Best Local Similarity:
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Alignment Scores:

Query Match: DB:

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152 TCAGGAAGCAACACTTIGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT 211
                                                             212 CAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTCAAAACCACA 271
                                                                                                      272 GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331
                                                                                                                                                                                                                                                                             Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TLE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
                                                                                   GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu
                                          GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr
                                                                                                                                                                                                                                                         Membrane-bound protein PRC1159 encoding cDNA.
                                                                                                                                                 GCCTGGGGCAGGGCTGTAAAGAAAAACACT 361
                                                                                                                            AlaTrpGlyArgGlyValLysLysAsnThr 90
                                                                                                                                                                                            AAZ65094 standard; cDNA; 713 BP
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98US-0088655P.
98US-0088722P.
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98US-0088825P.
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04-JUN-1998;
04-JUN-1998;
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11-AUG-1998;
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      98US-0096329P
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(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK; Wood WI, Yuan \mathcal{I}_i

WPI; 2000-072883/06.

P-PSDB; AAY66748

Membrane-bound proteins and related nucleotide sequences

Claim 2; Fig 271; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as plarmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	6.04e-52	Length:	713
	462.00	Matches:	90
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Ouery Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-989-293A-377 (1-90) x AAZ65094 (1-713)

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211
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MetThrPhePheLeuSerLeuLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn
                                                                                  SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
                                                                                                                        TCAGGAAGCAACACTTGGAGAATGGCTACTTTCTATCAAGAATAAAGAGAACCACAGT
                                                                                                                                                                       GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr
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20-APR-1999;
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15~SEP-1999;
05-OCT-1999;
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26-JUL-1999;
28-JUL-1999;
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10-MAR-1999;
12-MAR-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agoniets and antagonists are useful for treating and disquosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rhenmatod arthritis, selected from systemic lupus erythemators when arthritis, spondyloarthropathies, costeoarthritis, juvenile chronic arthritis spondyloarthropathies, systemic sclerosis, idiopethic inflammatory myopathies, Sjogran's systemic vasculitis, sarcoidosis, autoimmune hemolytic syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic syndrome, systemic hemolocytopaenia, thyroiditis, diabetes mellitus, limmune-mediated ranal disease, demyelinating diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune cor immune-mediated skin diseases, allergic diseases, immunological cor immune-mediated skin diseases, allergic diseases, immunological cor immune and graft-versus-host-disease. AACS8337 to AACS8578

Crepresent PRO sequences AACS8579 to AACS8642 and AAB33414 to AAB33477

crepresent human PRO polynucleotide and protein sequences given in the crepresent human PRO sequences invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL, Hebert C, Henzel W; D, Shelton DL, Smith V; Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ, Baker KP, Goddard A, Gurney AI
Kabakoff RC, Lu Y, Pan J, Pennica D, Sheltc
Stewart TA, Tumas D, Watanabe CK, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Fig 111; 309pp; English.
                                                                                                                                                                                                              2000WO-US000219.
2000WO-US000277.
2000WO-US000376.
2000WO-US004341.
2000WO-US004342.
             99WO-US028214.
99WO-US028313.
99WO-US028409.
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11-FEB-2000;
                                                30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
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92

1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn

US-09-989-293A-377 (1-90) x AAC58634 (1-713)

8 B 8

713 90 0 0 0

Matches: Conservative: Mismatches:

Indels:

Length:

6.04e-52 462.00 100.00% 100.00% 100.00%

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Percent Similarity: Best Local Similarity:

Query Match: DB: 20

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                                                                                                                                                                                           Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                          GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331
152 TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACGT 211
               GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
                                               GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
                                                                                                                                                                              Human cDNA sequence encoding for PRO1159 polypeptide.
                                                                                         GCCTGGGGCAGGGTGTAAAGAAAAACACT 361
                                                                               AlarroglyArgGlyValLysLysAsnThr 90
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99WO-US028551.
99WO-US028564.
99WO-US028565.
99US-0170262P.
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2000WO-US004414.
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2000WO-US005841.
2000US-0187202P.
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99WO-US030911.
99WO-US030999.
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2000WO-US023522
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2000WO-US000277.
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2000WO-US003565.
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2000WO-US005004
                                                                                                                               AAS21480 standard; cDNA; 713
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                                                                                                                                                               (first entry)
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24-FEB-2000;
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02-MAR-2000;
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30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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18-FEB-2000;
22-FEB-2000;
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30-MAY-2000;
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17-MAY-2000;
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AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to madulate biological activities of cells expressing PRO comparate, to madulate biological activities of cells expressing PRO breast, prostate, rectal, cervical activities of cells expressing PRO breast, prostate, rectal, cervical or liver tumours by comparing PRO copypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour of fiferentiation of chondrocytes, the proliferation or agene expression in differentiation of chondrocytes, the proliferation of proliferation of inner ear utricular supporting cells or of Tromporties, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal colls or by adipocytes; or inhibit binding of A-peptide to factor viral, the PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The proloning interactions. The proloning interactions in the proloning interactions. The proloning interactions in the proloning interactions. The proloning interactions is the proloning interactions. The propose is a processing the processing interactions in the proloning interactions. The proloning interactions is the proloning interactions. The proloning interactions is the proloning interactions in the proloning interactions. The proloning interactions is the proloning interactions in the proloning interactions in the proloning interactions is the proloning interactions in the prolo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
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                                                                                                                                                                         (GETH ) GENENTECH INC.
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Best Local Similarity:
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P-PSDB; AAU12408
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WO200073454-A1

Homo sapiens.

02-APR-2001 AAF44240;

RESULT 5 AAF44240 30-MAR-2000;

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cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the stolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAF65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
                                                                                                                                                                                                                                                                                                                           GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu
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                                                                                                                                                                                                                                                                                                        MetThrPhePheLeuSerLeuLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn
                                                                                                                                                                                                                                                                                                                                                                       SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
                                                                                                   Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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97US-0062250P.
97US-0065186P.
97US-006511P.
97US-0065311P.
97US-0065311P.
98US-0075945P.
98US-0078910P.
98US-0084600P.
98US-0084600P.
98US-0087607P.
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05-NOV-1997;
12-NOV-1997;
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20-MAX-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells,
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                                                                                                                                                                           PRO; cytostatic; cell death; tissue typing;
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Wood WI;
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                                                                                                                                             SEQ ID NO:376
                                                                                                                                               Human PRO1159 (UNQ589) nucleotide sequence
                                                                                                                                                                            secreted and transmembrane protein; chromosomal mapping;
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                                               AAF44240 standard; cDNA; 713
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P-PSDB; AAB65271.
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06-JAN-2000; 11-FEB-2000; 18-FEB-2000; 22-FEB-2000;

24-FEB-2000; 02-MAR-2000;

Roy MA, Zhang Z

24-FEB-2000;

20-DEC-1999; 05-JAN-2000;

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17-AUG-1999;

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2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
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18-FEB-2000; 2
24-FEB-2000; 2
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2003-247083/24.
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                                     17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
28-JUL-2000;
                                                                                                   Ashkenazi AJ,
                                                            24-AUG-2000;
08-NOV-2000;
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                      LO-MAR-2000;
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20-MAR-2000;
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                               30-MAR-2000;
                                   15-MAY-2000;
      18-FEB-2000;
        22-FEB-2000;
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2000WO-US032678 2001WO-US006520 2001WO-US017800 2001WO-US021066 2001WO-US021735 2001US-00941992 2000WO-US023328 2000WO-US030952 2000WO-US004914 2000WO-US005004. 2000WO-US005841. 2000WO-US006319 2000WO-US014042 2000WO-US022031 000WO-US006884 2000WO-US007377 2000WO-US008439 2000WO-US013358 2000WO-US013705 2000WO-US014941 2000WO-US015264 2000WO-US020710 2000WO-US023522 (GETH) GENENTECH INC.

Godowski PJ; Paoni NF; Wood WI; Baker KP, Botstein D, Desnoyers L, Eaton ng S, Gerber H, Gerriteen ME, Godard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, att TA, Tumas D, Watanabe CK, Williams PM, Ferrara N, Fong S, Grimaldi JC, Gurney Roy MA, Stewart TA,

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer

Claim 2; Fig 273; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus collypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 or PRO943, PRO926, PRO1066 or PRO535, PRO626, PRO819, PRO1136, and PRO1367 induce c-fos in endothelial growth, and PRO136, cuseful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular calculated T-lymphocytes and art ethnis polypeptide are cells and is thus useful for inhibiting endothelial cell growth in mannals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing cimmune response. PRO826, PRO132 is also enhances survival/proliferation of immune response. PRO826, PRO132 is also enhances survival/proliferation of individual coll growth in the coll production of individual colls and therefore are useful for treating retainal colls and therefore are useful for treating retainal colls and processes are useful for treating retainal colls and processes are useful for mannals processed to the processes and are therefore are useful for treating retainal colls and therefore are useful for treating retainal colls and processes and are therefore are useful for treating retainal colls and processes are useful for treating retainal colls and processes and therefore are useful for treating processes and colls and colls. disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammalian Kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the

02-JUN-1998;

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GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331
                                                                                                                                                                                                                                                                            211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; gene; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.
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proliferation and/or redifferentiation of chondrocytes in culture and a thus useful for treating sports injuries, and arthritis. This sequence represents a novel human FRO protein polynucleotide
                                                                                                                                                                                                               92 AIGACATTTTTTCTGTCACTATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAT
                                                                                                                                                                                                                                                    SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
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                                                 Other;
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Matches:
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Indels:
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15-MAR-2000; 2
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 Human; secreted and transmembrane protein; PRO; antiinflammatory; antiateriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (TMF)-alpha release; TMF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; acardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing; gene; ss.
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Matches:
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2000WO-US006319.
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2001WO-US006520.
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2001WO-US021066.
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2001US-00828366.
2001US-00854208.
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2001US-00887879
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2001US-00808689
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Stewart TA,
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 28-FEB-2001; 2
28-FEB-2001; 2
01-MAR-2001; 2
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                                                    14-MAR-2001; 22-MAR-2001; 205-APR-2001;
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18-MAY-2001;
25-MAY-2001;
25-MAY-2001;
25-MAY-2001;
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18-JUL-2001;
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Smith V,
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Filvaroff E, Gao W; Deforge L, Desnoyers L, Filvaroff E, G: A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency syndrome (AIDS), or cancer.

Claim 2; Fig 473; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding or polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptide, laborative molecule to a cell expressing a propertied, modulate a biological activity of a cell, stimulate the PRO polypeptide, modulate a biological activity of a cell, stimulate the crease of tumour necrosis factor (TNF)-alpha from human blood, modulate the uptoliferation or differentiation of cells, stimulate the release of proteoglycans, stimulate the release of cytokine to proliferation or differentiation of cells or gene expression, the proliferation of differentiation of cells, shimilate the release of cytokine computed mononuclear cells, inhibit the binding of A-peptide cofficed and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, diseases, organ failure, atherosclerosis, cardiac injury, infertility, diseation probes, in chromosome and gene mapping, and in generating complisers RNA or DNA. The polypeptides are useful as pharmaceuticals, antisense RNA or DNA. The polypeptides are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PNO

Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

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92 Arcacarritricrorcactarrarrarrorrigaadergaactarricoagarcaar 151
                                                                                                                                                212 CAACCCACACAATCATCTTTAGAAGACAGTGTGACCCTACCAAAGCTGTCAAAACCACA 271
                                                                                                                                                                                                                                  272 GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331
                                                                                                                                                                       GlnProThrGlnSerSerLeuGluAspSerValThrProThrlysAlaValLysThrThr 60
                                                                                                                                                                                                              61 GlyLysGlyTlevalLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
                                                                                                                                40
                                                                                          MetThrPheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn
                                                                                                                                SerglySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; ss; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.
    7113
90
0
0
0
                                                                                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane protein cDNA, #154.
                        Conservative:
Mismatches:
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     Length:
Matches:
                                             Indels:
                                                                                                                                                                                                                                                         81 AlaTrpGlyArgGlyValLysLysAsnThr
                                                                        (1-713)
                                                                          US-09-989-293A-377 (1-90) x ACD24089
                                                                                                                                                                                                                                                                                                                     ABX90341 standard; cDNA; 713 BP
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98US-0087106P.
98US-008707P.
98US-0087759P.
98US-0088021P.
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98US-0088028P.
98US-0088028P.
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98US-0078910P.
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97US-0066770P.
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04-JUN-1998;
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Alignment Scores:
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98US-0089612P.
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99WO-US005028.
99WO-US012552.
99WO-US021090.
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99WO-US030095.
99WO-US030911.
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2000WO-US004914.
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99WO-US028313.
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11-FEB-2000; 2
18-FEB-2000; 2
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24-FEB-2000; 2
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110-MAR-2000;
20-MAR-2000;
30-MAR-2000;
115-MAY-2000;
117-MAY-2000;
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28-JUL-2000;
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28-AUG-2001;
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16 - 70N - 1998;
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17 - 70N - 1998;
17 - 70N - 1998;
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16-SEP-1998;
17-SEP-1998;
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01-DEC-1998;
05-JAN-1999;
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10-JUN-1998;
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332 geeregegekegereraakaaaakeker 361

ВЪ

ABX64187 standard; cDNA; 713

ABX64187;

ABX64187
ID ABX6
XX
AC ABX6

81 AlarrpGlyArgGlyValLysLysAsnThr 90

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The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid conding them. The polypeptides can be used to raise antibodies that encoding them. The polypeptides can be used to raise antibodies that compenied to a cell expressing a PRO protein and for modulating at least concloude to a cell expressing a PRO protein and for modulating at least concloudes are also useful in gene therapy, in chromosome. The PRO plypeptides or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, collypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing and the isolated nucleic acids may be used for recombinantly expressing concluse typing. Anti-PRO antibodies are useful in diagnostic assays for tissue typing. Anti-PRO antibodies are useful in diagnostic assays for those markers. The Sequences presented in ABX90083-ABX90468 are the natural sources. The sequence in ABX90083-ABX90468 are the polymucleotides of the invention. Note: The sequence data for this patent constitution of the probes detecting the PRO polymucleotides of the invention. Note: The sequence data for this patent constitution of the probes detecting the PRO sequence. The RDA probes detecting the PRO sequence. The sequence of the invention.
                               Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                   New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 271; 650pp; English.
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(GETH ) GENENTECH INC
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The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
biological activities of cells expressing PRO polypeptides, and for in
closedical activities of cells expressing PRO polypeptides, and for for
closedical activities of cells expressing PRO polypeptides, and for for
closeding PRO polypeptides are useful as hybridisation probes, in
chromosome and gene mapping, in the generation of antisense RNA and DNA,
in the preparation of PRO polypeptide, for generating transgenic animals
or knockout animals, to construct hybridisation probes for mapping the
created an encodes the PRO polypeptide, and for generic analysis of
individuals with genetic disorders, in gene therapy, for chromosome
identification, as chromosome markers, and for generating probes for PCR,
Northern analysis, Southern analysis and Western analysis. The present
sequence encodes a human PRO polypeptide of the invention. Note: The
sequence data for this patent was obtained in electronic format directly
from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
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Human, PRO polypeptide, secreted protein, transmembrane protein, genetic disorder, antibacterial, immunosuppressive, transgenic, gene therapy, gene; ss.
                                         cDNA encoding human PRO1159 polypeptide
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98US-0087603P
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98US-0088021P
98US-008802E
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           26-FEB-2003 (first entry)
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13-NOV-1997;
13-NOV-1997;
25-FEB-1998;
20-MAR-1998;
07-MAR-1998;
07-MAY-1998;
02-JUN-1998;
02-JUN-1998;
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n DL;
Godowski PJ;
Paoni NF;
M. Wood WI;
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2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004341.
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2000WO-US013358.
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02-JUN-2000; 2
28-JUL-2000; 2
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18-FEB-2000;
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 06-JAN-2000;
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Zhang Z;
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9705 - 0062814P

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9705 - 0063082P

9705 - 006332P

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03-NOV-1997;
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31-MAR-1998;
12-JUN-1998;
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23-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, PRO polypeptide, secreted and transmembrane protein, anti-PRO antibody, diagnostic assay; gene expression, diabetes, bone disorder; cartiage disorder; rheumatoid arthritis, obesity, sports injury; osteoarthritis, hyper-insulinaemia, hypo-insulinaemia, hearing loss; coaquilation disorder; stroke, heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
                                                                                                                                                     ATGACATTTTTTCTGTCACTATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAT
                                                                                                                                                                                                  TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAAACCACAGT
                                                                                                                                           1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn
                                                                                                                                                                                    SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
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          0 U; 0 Other;
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Matches:
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Mismatches:
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         134 G; 212 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human PRO polypeptide #237.
                                                                                                                   US-09-989-293A-377 (1-90) x ABX64187 (1-713)
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97US-0056974P.
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                                       6.04e-52
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          A; 105
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         Sequence 713 BP; 262
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17.SEP-1997;
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                               Alignment Scores:
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Human; secreted and transmembrane protein; cytostatic; anti-HIV; virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy; pRO; pharmaceutical; diagnostic; biosensor; bioracactor; malignancy; cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease; drug screening; gene; ss.
                                                                                                                                                                   Novel human secreted and transmembrane protein PRO1159 cDNA.
GCCTGGGGCAGGGGTGTAAAGAAAAACACT 361
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98US-0088126P
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98US-0088212P
98US-0088217P
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                                                                                                                                         (first entry)
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                                                                ACA64409
                                                                                                         The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA66994-AA67268 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web
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                                                                                                                                                                                                                                                                                                                                                   New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, heart attack.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                          2000WO-US004342.
2000WO-US004114.
2000WO-US0049114.
2000WO-US005004.
2000WO-US005601.
                                              2000WO-US000277.
2000WO-US000376.
2000WO-US003565.
2000WO-US004341.
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06-JAN-2000;
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11-FEB-2000;
18-FEB-2000;
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01-MAR-2000;
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Wart TA, Tumas D,
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Grimaldi JC, Gurney
Roy MA, Stewart TA,
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PJ; i, Eaton DL; ddard A, Godowski PJ Pan J, Paoni NF; liams PM, Wood WI; Goddard A, MA, Pan J, Williams PM, H, Gerritsen ME, Goddard Ljavin IJ, Napier MA, Pan D, Watanabe CK, Williams Desnoyers L, Baker KP, Botstein D,

WPI; 2003-352829/33. P-PSDB; ABU72562.

New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's disease

Claim 1; Fig 271; 663pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 522-pTA, 819-PTA, 209439, 203135, etc); or a sequence with a least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polymoclectides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These

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Human, PRO polypeptide, secreted and transmembrane protein, tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
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are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepatitis B, multiple solateosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
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The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking polypeptides are useful for detecting other PRO polypeptides, for linking biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TMF)-alpha from theman blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and CDNA, in the preparation of PRO polypeptides, for generating transpenic animals or knockout animals, for the genetic analysis of individuals with generating the human PRO polypeptides of the invention. Note: The sequence conding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
18-MAY-2001; 2001US-00860216.
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01-MAR-2000; 2
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    212 CAACCCACACATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGGTGTCAAAACCACA 271
GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGCTGAA 331
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                                  9
                                                                                                                                                                                                                                                                 Human, PRO; hypertrophy of neonatal heart; anglogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VBGF inhibition; retinal reurons cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herperiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
                                                                        GlyLysGlylleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu
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                                                                                                                                                                                                                                               DNA encoding novel secreted and transmembrane protein PRO1159.
                                                                                                                             81 AlaTrpGlyArgGlyValLysLysAsnThr 90
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29-OCT-1998;
29-OCT-1998;
20-NOV-1998;
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Gerritsen Smith V, Baker KP,

Gao W; Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, 1 ME, Goddard P Stewart TA, 1

WPI; 2003-148238/14.

P-PSDB; ABUS9887

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

Claim 2; Fig 473; 659pp; English

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in inking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus tusful for treating cardiac insufficiency discoders. PRO156, PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO343, PRO826, PRO168 or PRO535, PRO819, PRO1367, induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e-g. wound healing and antagonist of this polypeptide are useful for treating concerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGP) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO826, PRO1068, PRO1088, PRO826, PRO1068, PRO1132 is also enhances survival/proliferation of retinal neurons cells and therefore are useful for trating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813, and therefore are useful for treating kidney disorders associated with decreased mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are encodes a novel human PRO protein

Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

713 90 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 6.04e-52 462.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match:

US-09-989-293A-377 (1-90) x ABX89377 (1-713)

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1 MetThrPhePheLeuSerLeuLeuLeuLeuLeuValCysGluAlalleTrpArgSerAsn 20

	81 AlaTrpGlyArgGlyValLysLysAsnThr 90	86	à
331	272 GGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATTCTTGGTGTTGAA 331	273	qq
80	61 GlyLysGlylleValLysGlyArgAsnLeuAspSerArgGlyLeulleLeuGlyAlaGlu 80	9	δ
271	2 CAACCCACACAATCAICTIIIAGAAGACAGTGTGACTCCTACCAAAGCTGTCAAAACCACA	213	qq
09	41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60	14	δ
211	152 TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT 211	153	qq
40	21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40	21	QY
151			QC C

332 GCCTGGGGCAGGGTGTAAAGAAAAACACT 361

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4, 2004, 08:12:56 completed: April me : 433 secs Search cor Job time

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Copyright (c) 1993 - 2004 Compugen Ltd.
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AR252626 Sequence AX055452 Sequence AX403489 Sequence AX464340 Sequence AX358685 Homo sapi

Description

Homo sapi Homo sapi Novel membr Homo sapi AX912349 Sequence BD047882 Sequence AC13877 Rattus no AC123647 Rattus no AC128368 Rattus no AC126817 Rattus no AC141026 Rattus no AC095739 Rattus no AC133293 Rattus no AC09560 Rattus no

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AUTHORS TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 AIGACAITITITCIGECACIAITAITAITGIIGEGAIGAGGAAGCIAITIGAAGAICCAAI 151
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Genentech Inc. (US)
Location/Qualifiers
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AX403489
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer
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                                                                                                                                   Unclassified.

1 (bases 1 to 713)
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Implant, method of making same and use of the implant for the treatment of bone defects
Patent: US 6478825-A 376 12-NOV-2002;
Location/Qualifiers
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                  AR252626
Sequence 376 from patent US 6478825.
AR225626
AR252626.1 GI:27300534
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AX055452
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 713)

I (bases 1 to 713)

Clark.H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,

Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,

Dowd, P., Eaton, D., Foster, J., Gimaldi, C., Gu, Q., Hass, P.E.,

Heldens, S., Huang, A., Kim, H.S., Kilmowski, L., Jin, Y., Johnson, S.,

Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,

Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,

Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,

Goddard, A., Wood, M.I. and Godowski, P., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale

Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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                                                               AY358685 713 bp mRNA linear PRI 03-OCT-2003
Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.
AY358685
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CA 94080, USA
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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Genome Res. 13 (10), 2265-2270 (2003)
332 GCCTGGGGCAGGGTGTAAAGAAAAAACACT 361
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92 ATGACATITITICIGICACTATIATIATIGITGGIAIGIGAAGCIAITIGGAGAICCAAI 151
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AX464340
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KEYWORDS SOURCE

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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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/function="unresolved homopolymeric run"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Muc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
Worley, K.C.
Direct Submission
Submitted (26-MAY-2002) Human Genome Sequencing Center, Department
Submitted (26-MAY-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 165414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
                                                                                                                                                                                                                                                         Submitted (29-MAY-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Saylor Houston, TX 77030, USA On MAY 29, 2002 this Sequence version replaced gi:21206012.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
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/db xref="taxon:9606"
/chromosome="12"
/clone="RP!1-133L14"
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/rpt family="MIR"
complement(2987. .3137)
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/rpt_family="MER5A"
4859. .4941
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/rpt_family="MLT1D"
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family="(CA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANNOTATION OF FEATURES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  gc-help@bcm.tmc.edu
                                                                                                                                                                                              Worley, K.C.
Direct Submission
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10 (Dases 1 to 1654)

Marzoy, D. W. Adams, C., Adlo-Oduola, B., Ail-Oman, F. X. Ailen, C.,

Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,

Bunay, C., Burch, P., Catter, M., Cavazos, S. R., Chacko, J. Chavez, D.,

Catron, T. R., Catter, M., Cavazos, S. R., Chacko, J. Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C.,

Carron, T. R., Davis, C., Chiu, D., Chowdhry, I., Christopoulos, C.,

Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R.,

Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A.,

Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A.,

Bannar, C., Edgar, T., Ferraguto, D., Flaggy, N., Ford, J., Roster, P.,

Escotto, M., Falls, T., Ferraguto, D., Flaggy, N., Ford, J., Roster, P.,

Gall, R., Gorrell, J. H., Gao, J., Garcia, A., Garner, T., Garza, M.,

Gall, R., Gorrell, J. H., Gao, J., Harris, C., Harris, K., Hark, M., Havlak, P.,

Hamilton, K., Garrell, J. Harris, C., Harris, K., Hark, M., Havlak, P.,

Hume, J., Iolikhes, J., Harris, C., Harris, K., Hark, M., Havlak, P.,

Hume, J., Locikhes, T., Ferraguto, J., Kurseni, P., Jia, S.,

Hume, J., Locikhes, J., Memai, E., Wachson, B., Jia, Y.,

Johnson, R., Jolivet, S., Joudah, S., Karlson, B., Jia, Y.,

Liau, C., Liui, J. Liu, W., Loulseged, H., Lozado, R. J., Lu, K.,

Markiney, B., Mcredo, M., Parkins, C., Ludy, M., Martinez, E.,

Markiney, B., Mcredo, M., Martiner, G., Matchoria, S., Ravery, G.,

Manniney, E., Montegon, P., Marten, M., Martinez, E.,

Markiney, B., Monter, S., Oguh, M., Okrabon, S.,

Markiney, B., Mottodo, R., Payton, B., Peery, J., Perez, I.,

Rives, M., Molter, M., Pinner, S., Bacery, J., Perez, J.,

Perers, J., Montegon, E., Morten, R., Payton, B., Peery, J., Scherers, J., Stoker, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Raling, M., Marten, M., Raling, M., Marten, M., Marten, M., Sodergren, B., Sonte, A., Payton, 
                                                                                                                                                                                                                                                                                                                                                                 AC024224 165414 bp DNA linear PRI 29-MAY-2002 Homo sapiens 12 BAC RP11-133L14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
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                                                                                                272 gecaaggecaragrraaagacggaarcrrgacrcaagagggrraarrcrrggrgcrgaa 331
                                         80
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
                                      GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu
                                                                                                                                                                                                            332 GCCTGGGCAGGGGTGTAAAGAAAACACT 361
                                                                                                                                                                         90
                                                                                                                                                                         81 AlarroglyArgGlyValLySLysAsnThr
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AC024224.33 GI:21240476
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DEFINITION
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165414 90 0 0 0 Matches: Conservative: Mismatches: Indels: 462.00 100.00% 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: Score:

EMERATORIA MELERGA CATARTHINI'S HOMINIGAE'S HUTCHERORIAL MEMBRANDIA'S MELERGA CATARTHINI'S HOMINIGAE'S HOUGH MERATORIAL MENTALLAN'S MERATORIAL MERATORIAL'S ALBORNEY, MAISTONES, I., AMERCHURGH.H.C., ARE, T.R., BANKS, T., BADDATIA, J., ALBORNEY, S. HARCHOURGH, C., ARE, J.R., BANKS, T., BADDATIA, J., BUNGRE, K., BIANKENDOKE, S. L., AMERCHURGH.H.C., ARE, J.R., BANKS, T., BADDATIA, J., BUNGRE, K., BIANKENDOKE, CARTON, T.F., BUNCH, P., BURCH, P., BURCH, P., BURCH, C., CHOCK, J., CHONG, C., CARCON, C., CAROCAL, S., CHORADY, I., CHACKO, J., CHANGA, C., CHOR, R., CARTON, T., CHOWARY, I., CANTAGOROUGOS, C., CLEVELAND, C., CHORAGA, C., CHOR, R., DOUTHMAN, H., DAVIS, C., COX.C., DANY-CARTON, J., DANDEN, H., DAVIS, C., CANGO, DOUGH, M.D., DARIBA, T., EARIBART, ENTRANGA, C., CHORAGA, S., DURDIN, H.H., DOUTHWANTE, C., EGGAR, D., EBDAGO, DANY-CARTON, J., ENTRAIS, C., ERCALS, T., ENTRAIS, C., ERRAGATO, F. FARDER, C., ERCALS, T., CORTELL, H., GORTELL, H., GURCHOL, H., HAVIS, C., CHONGO, T., CH 117328 AIGACATTTTTTCTGTCACTATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAT 117269 117268 TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT 117209 Homo sapiens clone RP11-13C13, RP11-656B20, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces.
AC006510 AC006514
AC006510.8 GI:10122019 40 9 61 GlyLysGlylleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. MetThrPhePheLeuSerLeuLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 117088 GCCTGGGCAGGGGTGTAAAGAAAAACACT 117059 81 AlarrpGlyArgGlyValLysLysAsnThr 90 US-09-989-293A-377 (1-90) x ACC24224 (1-165414) HTG; HTGS_PHASE1. Homo sapiens (human) Homo sapiens RESULT 7 AC006510/c DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS 셤 셤 à 셤

REFERENCE

COMMENT

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211659 ATGACATTITITCTGTCACTATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAT 211600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211599 TCAGGAAGCACATTGGAGAATGGCTACTTTCTTATCAAGAAATAAAGAGAACCACAG 211540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 19-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.

1 (Dases 1 to 625)

Willment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 Thr-GlyLysGlylleValLys-GlyArgAsnLeuAspSer-ArgGlyLeuIleLeuGly 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 bp mRNA linear PRI 19-NOV-20
Homo sapiens beta-glucan receptor isoform C (BGR) mRNA, complete
cds, alternatively spliced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 r-GlnProThrGlnSerSerLeuGluAspSerValThrProThr-LysAlaValLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211539 recaececacacarrerrerradagacadrerereraceaaaagerereaaaace
                                                                                                                                                                                                                                                                                                                                                        1 MetThrPhePheLeuSerLeuLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                    21 SerGlySerAsnThrLeuGluAsnGlyTyr-PheLeuSerArgAsnLysGluAsnHisSe
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Willment, J.A., Gordon, S. and Brown, G.D.
Direct Submission
Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 AlaGluAlaTrpGlyArgGlyValLygLysAsnThr 90
                  1. .240864
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-13C13, RP11-656E20"
                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:9606"
/chromosome="12"
location/Qualifiers
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369.00
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Homo sapiens
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Best Local Similarity:
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AF400597
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Center clone name: RP11-13C13, RP11-656E20

Center clone name: RP11-13C13, RP11-656E20

Sequencing vector: Plasmid; M77789
Sequencing vector: M13; L08821
Chemistry: Dye-treminator Big Dye: 23% of reads
Chemistry: Dye-treminator Big Dye: 23% of reads
Chemistry: Dye-treminator Big Dye: 23% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 71554 bases at least Q40
Consensus quality: 93014 bases at least Q30
Consensus quality: 11072 bases at least Q20
Estimated insert size: 229041; sum-of-contigs estimation
Estimated insert size: 331000; agarose-fp estimation
Quality coverage: 0.6x in Q20 bases; sum-of-contigs estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
    Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
                                                                                                  Worley, K.C.
Direct Submission
Submitted (OS-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2000 this sequence version replaced gi:10086352.
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111185: gap of unknown length
134782: contig of 23597 bp in length
134862: gap of unknown length
163754: gap of unknown length
163754: gap of unknown length
185050: contig of 28772 bp in length
185050: contig of 21296 bp in length
185050: contig of 9652 bp in length
194902: gap of unknown length
202527: contig of 7625 bp in length
202527: contig of 7625 bp in length
202527: contig of 7625 bp in length
203585: gap of unknown length
203585: contig of 6031 bp in length
21785: contig of 6130 bp in length
21885: gap of unknown length
221885: gap of unknown length
230142: contig of 8357 bp in length
230142: contig of 8557 bp in length
230142: contig of 8557 bp in length
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of 1734 bp in length
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g of 1262 bp in length
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      Worley,K., Wu,C., Wu,Y.,
and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 240864)
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Aravusss
Homo sapiens beta-glucan receptor isoform A (BGR) mRNA, complete cds, alternatively spliced.
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1; alternatively spliced"
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1 (bases 1 to 744)
Willment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                          217 AATTCAGGAAGCAACACTTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AGICAACCCACAATCAICTIIIAGAAGACAGIGIGACICCIACCAAAGCIGIGAAAAAC 336
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Direct Submission
Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK
Location/Qualifiers
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Mismatches:
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  1. .741
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1; alternatively spliced"
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SNELISDQNHSYPRKPISKLCMDSRVSHL"
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unclassified.

l (bases 1 to 741)
Shuji, H., Shoji, F., Kazunori, N. and Yasushi, A.
Shuji, H., Shoji, F., Kazunori, N. and Yasushi, A.
Shuji, H., 1999001497-A 2 06-JAN-1999;
TAKEDA CHEM IND LTD
OS Unidentified
PN JP 1999001497-A/2
PD 06-JAN-1999
PF 13-UUN-1997 JP 1997156376
PR SHUJI HINUMA, SHOJI FUKUZUMI, KAZUNORI NISHI, Y.
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/organism='Unidentified'
Location/Qualifiers
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Mismatches:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 744)
Hermanz-Falcon, P., Arce, I., Roda-Navarro, P. and Fernandez-Ruiz, E.
Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene expressed on dendritic cells
Immunogenetics 53 (4), 288-295 (2001)
 /db_xref="G1:15986700"
/translation="MEYHPDLENLDEDGYTQLHFDSQSNTR1AVVSEKGSCAASPPWR
LIAVIIGILCIVILYIAVACHWAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLED
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SNELGFIVKQVSSQPDNSFWIGLSRPQTBVPWLWEDGSTFSSNLFQIRTTATQENPSP
NCVWIHVSVIYDQLCSVPSYSICEKKFSM"
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Direct Submission
Submitted (05-0cT-2001) Biologia Molecular, Hospital de la
Strincesa, Diego de Leon 62, Madrid 28006, Spain
Sequence update by submitter
On Oct 5, 2001 this sequence version replaced gi:14278818.
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Submitted (01-FEB-2001) Biologia Molecular, Hospital
Princesa, Diego de Leon 62, Madrid 28006, Spain
3 (bases 1 to 744)
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Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, B.
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Matches:
Conservative:
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Gaps:
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/organism="Homo sapiens"
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1. .744
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247.50
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/protein id="AAKZ0114.2"
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SNBLGFTVKQVSSSQPONSFWIGLSRPQTBVPWLWEDGSTFSSNLFQIRTTATQENPSP
NCVWIHVSVIYDQLCSVPSYSICEKKFSM"
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complete
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Millment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
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Willment, J.A., Gordon, S. and Brown, G.D.
Direct Submission
Submitted (18-JUL-22001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens beta-glucan receptor isoform G (BGR) mRNA, cds, alternatively spliced.
AF400601.
AF400601.
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                  /codon_start=1
/product="lectin-like receptor 1"
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Matches:
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/organism="Homo sapiens"
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/gene="DECTIN1"
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Homo sapiens
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Lipp,H.J., Mechtcheriakova,D., Schmid,J. and Sobanov,Y.
Ikk2 variant, dino gene, lectin-like receptor gene, and proteins
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Patent: WO 02077216-A 7 03-OCT-2002;
Novartis AG (CH) ; Novartis Erfindungen Verwaltungsgesellschaft
M.B.H. (AT)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 7 from Patent WO02077216.
AX664609
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Isolated mammalian membrane protein gene and reagent relating
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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JP 2002506645-A/3
05-MAR-2002
15-MAR-1999 JP 2000536856
17-MAR-1998 US 09/040111
LIONEL CHALUS,AHN QUAN, ELIZABETH ESTHER MARY BATES, DANIEL M
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Chalus.L., Quan, A., Bates, B.E.M., Gorman, D.M., Saeland, S.,
Lebecque, S.J.E. and Jr, J.H.P.
Isolated mammalian membrane protein gene and reagent relating
Patent: JP 2002506645-A 3 05-MAR-2002;
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SNBLGBTVKQYSSQPDNSFWIGLSRPQTBVPWIMEDGSTFSSNLFQIRTTATQENPSP
NCVWIHVSVIYDQLCSVPSYSICEKKFSM"
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Homo sapiens mRNA for DECTIN-1 receptor, splice variant 2.
AJ312373.
AJ312373.1 GI:14599395
alternative splicing, C-type lectin-1; DECTIN-1 gene; DECTIN-1
                       372 AATICAGGAAGCAACACATIGGAGAAIGGCIACTITCIAICAAGAAAIAAAGAGAACCAC 431
                                                                                                        432 AGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTCAAAAC 491
                                                                         59
20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submission (02-001) Vascular Biology and Thrombosis Research,
University of Vienna, Brunnerstrasse 59, Vienna A-1235, Austria
Alternative splicing: See also AJ312372.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrbini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NK gene complex, between CLEC-1 and LOX-1 genes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sobanov,Y., Bernreiter,A., Derdak,S., Mechtcheriakova,D.,
Duechler,M., Kalthoff,F. and Hofer,B.
A novel cluster of lectin-like receptor genes expressed in
monocytic, dendritic and endothelial cells maps close to the NK
receptor genes in the human NK gene complex
Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="C-type lectin-1"
/note="alternative splice variant 1 with stalk exon 3"
                                                                         SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr
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Mismatches:
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/gene="DECTIN-1"
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247.50
87.10%
80.65%
53.57%
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Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using frame_plus_p2n model nucleic search, OM protein

Run on:

April 4, 2004, 07:56:38; Search time 2701 Seconds (without alignments) 995.037 Million cell updates/sec 462 1 MTFFLSLLLLLVCEAIWRSN......DSRGLILGAEAWGRGVKKNT 90 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-989-293A-377 **BLOSUM62** score: Scoring table: Sequence: Title: Perfect :

27513289 segs, 14931090276 residues Searched:

Total number of hits satisfying chosen parameters:

55026578

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:*

Database :

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em_estin: *
em_estin: *
em_estov: *
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em_estin: *
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gb_est: *
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gb_est: * em_estfun:* gss mam: gss pro: em estom: * 1: em estba:* gss e Ę

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	escript	AU18577	4 CB95889	2 BI01896	9 AZ12145	AV721179	CB42081	BI10768	BE86562	BG16569	AL29042	BI91465	BH35433	BH354326	B0193507	BQ406117	CF735257	CG183911	CG457562	CC701258	CCI/1/03	CG691911	AG009588	CC616498	BG276251	1524 AGENCOURT BO920084 AGENCOURT	B08136 E	BF238075	BE723365	B1898668	CB457947	BF214995	BH198757	BU596994	BH135384	AL199104	BH123205	AA614424 1	BISS	BX346820	BQ721671	CG753752	AV827009 1	CC615145 OGVAG7	AC LINTIN LCCCCLAD
SUMM	OI .	AU18577	CRAFAR	BI0189	3 AZ1214	AV7211	1 CB420	2 BI107) BE865	2 BG165	9 CNS04	2 BI914	9 BH354	3 BH354	2 BJ193	3 BQ406	4 CF735	9 CG183	9 CG457	9 CC701	CC173	9 06691	AG005	9 00616	2 BG276	A2824	3 B081	D BF238	0 BE723	2 BI898	4 CB457	0 BF214	8 BH196	3 BU596	BH13	9 CNS07	8 BH123	AA614	2 BISS:	3 BX346	3 BQ723	9 CG753	AV827(9 CC615	, 0700
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ALIGNMENTS

AU185777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens CDNA clone B02302-019, mRNA sequence. AU185777.1 GI:14623690 AU185777/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

RESULT 1

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 663) Homo sapiens (human) Homo sapiens REFERENCE

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втолвую 2
IL3-MT0267-050101-437-A02 MT0267 Homo sapiens CDNA, mRNA sequence.
BI018962
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ammanlai; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 659)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 TCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 ATGACATTTTTCTGTCACTATTATTATTGTTGGTATGTGAAGCTATTTGGAGATCCAAT 401
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   http://image.llnl.gov
Plate: NDCMLs row:
High quality sequence stop: 488.
Location/Qualifiers
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Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 29-APR-2003
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1. (Dases 1 to 800)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon202-019"
/clone="B02302-019"
/cell_type="Mast cell"
/clone_lib="Homo sapiens Mast cell library (Sugita Y)"
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                                                                                     Kawasaki, Kanagawa 216-0001, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGENCOURT 13785021 NIH MGC_184 Homo sapiens cDNA clone IMAGE:30352338 5', mRNA sequence.
                                                                                                                                     URL: http://www.genox.co.jp
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   Sugita, Y., Oshida, T. and Oya, Y.
Human cDNA sequencing
Unpublished (2001)
                                                Contact: Yuji Sugita
Genox Research, Inc.
907 Nogawa, Miyamae-ku, Kawasab
Tel: 81-44-797-2281
Fax: 81-44-797-2622
Email: syuji@genox.co.jp, URL:
Email: syuji@genox.co.jp, URL:
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CB958894
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FEATURES

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/lab host="MH10B"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Morgan: Kidney/Brain, Vector: pBACe3.6; Site_1:
brote="Morgan: Kidney/Brain, Vector: pBACe3.6; Site_1:
brote lib = EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
brain genomic DNA was isolated and BcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PheLeuSerLeuLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySer 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 AGCACGAAAGGAGC-AATGGGATCCCGGATTCCAGAGGTTCATTTCCTGGTGCTGAGGCC 13
                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                   Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 IleVallysGlyArgAsn-----LeuAspSerArgGlyLeuIleLeuGlyAlaGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGlyLysGly
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-663)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="RPCI-23-30A15"
                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 663)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5e-16
209.00
69.51%
60.98%
45.24%
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RPCI-23-30AIS.TV RPCI-23 Mus musculus genomic clone RPCI-23-30AIS, genomic survey sequence.
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="makan" reference / mol type="makan" reference / mol type="makan" reference / mol type="makan" reference / mol the marrow, Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Luddig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amphification were performed under low
                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-MTO267-
050101-437-A02&t3=2001-01-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 639.
Location/Qualifiers
1. 659
//crganism="Homo" sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 AATTCAGGAAGCAACACATTGGAGAAATGGCTACTTTCTATCAAGAAAATAAAGAGAACCAC 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 AGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTACCAAAGCTGTGAAAACC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GlualaileTrpargser
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                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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AZ121459.1 GI:7788387
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247.50
87.10%
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Query Match: DB:

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Envises 1 to 582)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4300
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred vo.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match vo.990329.

Plate: PCY804 1 row: B column: 7
Seq primer: GTAATACGACTCATAGGG.
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602891529F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:5036647 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 CTGTTGAAGAGTGACAGCTTTCCATCAAGAAATAAAGACAACCAAGAGTCAACCCACACAA 333
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 855)
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                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab.host="MARC 6BOV"
/clome_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled From multiple tissues
including liver: lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LeuSerLeuLeuLeuValCysGluAlaileTrpArgSerAsnSerGlySerAsn
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 SerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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                                                                                                                                                                                                                                                                                                                                                          taurus"
                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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BI107684
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BI107684
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Bos taurus
Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                             AV721179 HTB Homo sapiens CDNA clone HTBAKF11 5', mRNA sequence.
AV721179
                                                                                                                                                                                                                                                                                                                                        Hu, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCACACAATCATCTTTAGAAGACAGTGTGACCCTACCAAAGCTGTCAAAAACCACAGGG 121
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                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I. (bases 1 to 673)

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X. Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, I., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R. Chen, J., Chen, Z. and Han, Z.

Homo sapiens CDNA HTB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLM"
/clone_lib="Hyps"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hars@eNgoc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 ProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB420818 582 bp mRNA linear
593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
CB420818
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HTBAKF11"
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                                                                                                                                                                     AV721179.1 GI:10818331
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100.00%
100.00%
44.59%
                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
Query Match:
83
                               7
TrpGly
                                   TGGGGT
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VERSION
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                                                                                                                               DEFINITION
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JOURNAL
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AV721179
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us-09-989-293a-377.rst

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/tissue type="carcinoma, cell line"
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/tlab_host="DH10B (T1 phage-resistant)"
/clone lib="NTH MGC 53"
/clone lib="NTH MGC 53"
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Site_1: Sfil (ggcgcctcggcc); Site_2: Sfil
(ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptors sequence: 5'-CACGGCCATTATGGCC-3' and 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 5'-ATTCTAGAGGCCGAGGCGGCCGATG-4T(30)BN-3' (where B = A, 5' or G and N = A, C, G, or T). Average insert size 1.55
kb (range 0.9-4.0, kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                             organism="Homo sapiens"
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/clone="IMAGE:3960715"
Location/Qualifiers
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BG165693.1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 GCATTATGGAGACACAATTCAGGGAGAAATCCAGAAGAGAAAGACAACTTCCCATCAAGA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AlalleTrpArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 833)
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Tissue Procurement: ArCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM843 row: k column: 20
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1101 row: j column: 08
High quality sequence start: 27
High quality sequence stop: 825.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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28
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Matches:
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138.50
74.47%
59.57%
29.98%
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Divaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dasses I to 924)
NIH-MGC http://mgc.nci.nih.gov/;
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CODNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Libr at:
http://image.llh.gov
Plate: LLAM10246 row: h column: 03
High quality sequence stop: 703.

High quality sequence stop: 703.
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602344512F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4454450 5',
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                                                                                                                                                                                                                                                                                                       LysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLys 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 LeuAspSerArgGlyLeuIleLeuGlyAlaGluAlaTrpGlyArg 84
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Direct Submission
Submitted (12-ARR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis elenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         979 ACCAGTTTTTGGGTGGGGAAGTAGGATAATCTCTGGCCGGAATCTTGGCTCTGAA 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            859 TAAACGTGTGAGAACTGATAGTAAAAGGGAGCCACGGCTTCAGCTTACCTGCTCAGGTGT 918
            Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GluAlaIleTrp 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1121
/organism="Tetracdon nigroviridis"
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/db_xref="tetracon:99883"
/clone="109N19"
/clone lib="G"
/note="Genoscope sequence ID : COBG109CG10LP1~end : T7"
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Homo sapiens
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Best Local Similarity:
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                     AUTHORS
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                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="INAGE="Hypernephroma, cell line"
/tissue_type="Thi08 (phage-resistant)"
/clone_lib="NIH MGC 89"
/note="Grgan: Xidney, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Mismatches:
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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CH230-163F15.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-163F15, genomic survey sequence.
                                                                                                                                                                                                                                                            Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

Clones are derived from the rat BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

Chtp://www.chori.org/bacpac/or ering information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 163 row: F column: 16

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear GSS 03-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 GGGAGAAACTAATGCTTCCAACACAGACCATCAGTGGAAAACTGCTTÄTGTGCAGGCAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
/cell type="Brain"
/clond lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: BcoRI; Site 2: BcoRI;
/note="Vector: pTARBAC4.1; Site 1: bcoRI; Site 2: BcoRI;
EHORI-230 Rat (BN/SENH8d/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LeulleLeuGlyAla 79
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 ThriysAlaValiysThrThrGlyLysGlyIleValLysGlyArgAsnLeuAspSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 ArgAsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro
                                           Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-163F16.TV
Ocher GSSs: Ch3mo
Department of Enkaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The 138 0208
The 138 0208
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-163F16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 GlualaTrpGlyArgGlyValLysLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-989-293A-377 (1-90) x BH354332 (1-391)
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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BH354326.1 GI:17285060
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79.00
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Best Local Similarity:
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COMMENT
    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="INGRESEATOR"
/clone="INGRESEATOR"
/lab host="DH10B"
/clone=lib="UNHH MGC 121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 25 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH354332 CH230-163F16.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-163F16, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 CACCAGCAATGCAGTCGGGCATCAAGGCTCAGTGTCTGGGACAGTCGTACCTAGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
Plate: LiAMISI4 row: p column: 10
High quality sequence stop: 668.
Location/Qualifiers
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                                                             MIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-683)
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Rattus norvegicus
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                                                                                                               Unpublished (1999)
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Best Local Similarity:
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Physicomitrella patens subsp. patens
Physicomitrella patens subsp. patens
Physicomitrella patens subsp. patens
Physicomitrella patens subsp. patens
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funarildae; Funariales; Funariaceae; Physicomitrella.
1 (Dases I to 536)
Nishiyama, T. Kamita, T. Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, T., Kujita, T., Shin-i, T., Seki, M., Nishide, H.,
Vohiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Kohara, Y. and Hasebe, M.
Comparative genomics of Physicomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 Adreachaceachachterageachad -----rachachterangeachterachte 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"

/sub species="patens"

/db_xref="taxon:145481"

/db_xref="taxon:145481"

/clone="pphn19n02"

/tissue type="mixture of chloronemata, caulonemata and rhizoid-like proconemata"

/clone lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Physcomitrella patens subsp. patens"
                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
22709184
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228
112
36
112
                                                                                                                                                                                                                                                                                                                                                                                     1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
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National Institute of Genetics
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                    GI:18361441
                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-559-81-6855
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79.00
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                                                                     Shao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shaartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-163F15.TV
Contact: Shaying Zhao.
Tother GSSs: CH230-163F15.TV
Contact: Shaying Zhao
Contact: Shaying Zhao
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Chtp://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Piters de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
Page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 163 row: F column: 15
Seq primer: Sp6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear EST 21-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 TCTAAGTTAAACAAAAGTCCGGGTCGTGGGGCTACTGATAGTGAGAAACAGAGGAATCTAAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 GGGAGAAACTAATGCTTCCAACACAGACCCTCAGTGGAAAACTGCTTATGTGCAGGCAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AGGGGTTCCTGTAATTTCTCTCTTTCACATCTCAGTCCTCATGCTCTGACAATATCACTATT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 ArgAsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro 53
    Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LeuIleLeuGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ193507 BF BB193507 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physocmitrella patens subsp. patens cDNA clone pphn19n02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 ThriysAlaVallysThrThrGlyLysGlylleValLysGlyArgAsnLeuAspSerArg
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 GAGGTGTTTGGAAGAGGGGGGGGGAAG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlualaTrpGlyArgGlyValLysLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10116"
/clone="CH230-163F15"
  Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                             (bases 1 to 504)
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31.88%
17.10%
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Best Local Similarity:
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Pred. No.:
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BJ193507/c
LOCUS
DEFINITION
                                                                                                                                       TITLE
JOURNAL
COMMENT
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

I (bases 1 to 641)

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

U unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Fax: 864 656 4293
                                                                                                                                                                                                                                                               BQ406117 G44 bp mRNA linear EST 22-MAY-2002 GA EG0090H12f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA Ed0090H12f, mRNA sequence.
BQ406117 GI:21093804
EST.
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235 GGCGAA------CAGGGAAGGCCAGTATCCCTCAACTGAGACATTCGCGGCTTTAAC 185
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41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gossypium arboreum"
/mol_type="mRNA"
/strain='AKA"
/cultivar="8400"
/db xref="taxon:29729"
/clone="GA_Ed0090H12f"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_l: EcoRI; Site_2: XhoI"
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18
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total High Quality bases = 584
Seg primer: TAAAGCACTACACTAAGGG
High quality sequence stop: 629.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-989-293A-377 (1-90) x BQ406117 (1-644)
                                                                                                                                                                                        184 CAAAGCAGCGATCTTGTCGGCCGT 161
                                                                                                                                                    77 LeuGlyAlaGluAlaTrpGlyArg 84
                                                                            GlyLysGlyIleValLysGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
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79.00
46.15%
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Best Local Similarity:
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                                                                            61
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BQ406117
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370 CAGCAGGCACTGCCTTCAGGATCATCAACTTCAACGTCAGTGTTGTCATTGTGTTCTCCA 429
                                                                                                                           430 GITACICCIGCIAAIACIGGCACCACIGCAAAGGCIGIA---GITGCIGCIGCI 486
                                                          ---ThrProThrLysAlaValLysThrThrGlyLys 62
                                                                                                                                                                                                                                      487 GGTAATATGAAAGGTGGTGGCATAGCATCACAGGGACTTATACATGCTGCACAA 540
                                                                                                                                                                                             63 GlyllevallysGlyArgAsnLeuAspSerArgGlyLeulleLeuGlyAlaGlu 80
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Search completed: April 4, 2004, 09:54:24 Job time : 2717 secs

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March 31, 2004, 12:07:55 ; Search time 14 Seconds
(without alignments)
334.737 Million cell updates/sec
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462
1 MTFFLSLLLLLVCBAIWRSN......DSRGLILGAEAWGRGVKKNT 90
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                          141681 segs, 52070155 residues
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                        Title:
Perfect score:
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                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                        Searched:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

141681

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries .

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

iption	099376 rattus norve 052349 mycoplasma P64796 human papil QBm9v0 chaetosphae P4803 homo sapiem P32562 saccharomyc P50090 saccharomyc P50090 saccharomyc 093266 agalychnis 093864 pachysolen Q55218 synechocyst Q58295 methanococc Q94414 xenopus lae Q96519 saccharomyc P19075 homo sapiem Q28509 macaca mula P2367 penicillium P2367 penicillium P2367 penicillium P2367 penicillium P34414 gallus gallu G6281 homo sapiem Q4444 gallus gallu G6781 homo sapiem Q4444 gallus gallu G6781 homo sapiem Q7994 musca domes Q88222 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P24386 homo sapiem P37806 caenorhabdi Q8734 pseudomonas
SUMMARIES	TERI RAT RSS_MYCGA RR3_CHGA RR3_CHGAC GALC_HUMAN CDCS_YEAST CDCS_YEAST CDCS_YEAST DNS6_AGAAN FRM1_AERPE MREA_XENLA CWFM_SCHPO TWM6_YEAST TYAS_HUMAN RAEA_YEAST TASS_HUMAN RAEA_YEAST TASS_HUMAN RAEA_RUMAN RAEA_R
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	622 226 226 226 802 802 803 803 803 803 803 803 803 803 803 803
% Query Match	44.44.44.44.44.44.44.44.44.44.44.44.44.
Score	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Result No.	1

P93568 solanum tub	P50282 rattus norv	Q9xdl1 bacillus th	P75280 mycoplasma	P21657 saccharomyc	Q10407 schizosacch	Q51330 oxalobacter	Q43923 acinetobact	Q12600 candida tro	Q58405 methanococc	P16535 pasteurella	P55116 pasteurella
UGS2 SOLTU	MM09 RAT	Clid_BACTU	YF06 MYCPN	DA81_YEAST	MKH1_SCHPO	OXLT_OXAFO	QUIX_ACICA	SIS2 CANTR	THS METUA	LKAI PASHA	LKA3_PASHA
Н	H	H	~	г	Н	Н	ч	~	ŧΗ	4-4	rl
641	708	719	793	970	1116	417	439	531	542	953	953
12.8	12.8	12.8	12.8	12.8	12.8	12.7	12.7	12.7	12.7	12.7	12.7
59	59	59	59	59	59	58.5	58.5	58.5	58.5	58.5	58.5
4.	35	36	3.7	88	68	0	덛	2	£3	44	5

ALIGNMENTS

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Local
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                                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                              207 LFKNMEGNCPPSWNIDSSCKLELSQNQNVKLTVNNVLKETRILNIFGVIKGYEEPDRYIV 266
                                                                                                                                                                                                                                            32 LSRNKENHSQPT---QSSLEDSVTPTKAVKTTGK------GIVKGRNLDSRGLI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20325869; PubMed=10867916; Skamrov A.V., Gol'dman M.A., Fecktistova E.S., Bibilashvili R.S.; Wetermination and analysis of the nucleotide sequence of a segment of a Mycoplasma gallisepticum strain A5969 chromosome, containing operons S10 and rrn23-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F., Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
"The complete genome sequence of the avian pathogen Mycoplasma gallisepticum strain R(low).";
Microbiology 149:2307-2316[2203)
-i- FUNCTION: With S4 and S12 plays an important role in translational accuracy (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and S8 (By similarity).

DOMAIN: The N-terminal domain interacts with the head of the 30S subunit; the C-terminal domain interacts with the body and contacts protein S4. The interaction surface between S4 and S5 is involved in control of translational fidelity.

SIMILARITY: Contains 1 S5 DRBM domain.
SIMILARITY: Belongs to the S5P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Located at the back of the 30S subunit body where it stabilizes the conformation of the head with respect to the body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S4
                                                                                                                                                                                                              23; Indels 17; Gaps
                                          LIGAND-BINDING (BY SIMILARITY).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (BY SIMILARITY).
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma gallisepticum.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
                                                                                                                                                                                 DB 1; Length 622;
                                                                                                                                          LINKED (GLCNAC. . .) (B)
831E4FC16DE55703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
15-Sos ribosomal protein S5.
RPSE OR RPSS OR MYCGA0680 OR MGA_0737.
                                                                                                                                                                                                                                                                                                                                                                                                              226 AA.
               Endocytosis, Phosphorylation.
                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                Pred. No. 11;
                                                                                                                                                                                14.8%; Score 68.5; 27.6%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STÄAIN=R(low);
MEDLINE=22830409; PubMed=12949158;
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                   70152 MW;
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267 VGAQRDAWGPGVAKSS 282
                                                                                                                                                                                                                                                                                                       77 LGA--EAWGRGVKKNT 90
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                              622
510
109
113
179
589
                                                                                                                                                                   Query Match
Best Local Similarity
....hes 21; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                   622 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A5969Var.B;
                                            431
508
109
113
179
584
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                   Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                         RS5 MYCGA
052349;
                                                                                                          CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SNSGSNTLENGYFLS--RNKENHSQPTQSSLEDSVTPTKAVKTTGKGIVKGRNLDSRGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=9265501; PubMed=8205838;

Delius H., Hofmann B.;
Primez-directed sequencing of human papillomavirus types.";
Primez-directed sequencing of human papillomavirus types.";
Primez-directed sequencing of human papillomavirus types.";

-I. FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
-I. FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
-I. FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
-I. FUNCTION: COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPRINDING OF E22R'S POSTITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INTITATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%; Score 67; DB 1; Length 226; 28.0%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type 52.
Viruses, dsDNA viruses, no RNA stage, Papillomaviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                             A -> V (IN REF. 1).
H -> R (IN REF. 1).
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01-UUN-1994 (Rel. 29, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Regulatory protein E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                HAMAR, MF 01307; -; 1.
InterPro; IPR000851; Ribosomal S5.
InterPro; IPR005712; Ribosomal S5.
InterPro; IPR005712; Ribosomal S5 b/o.
Pfam; PF00333; Ribosomal S5, 1.
Pfam; PF03719; Ribosomal S5, 1.
IGRPAMs; TIGR01021; TPSE Dact; 1.
PROSITE; PS00885; RIBOSOMĀL S5; 1.
                                                                                    EMBL; AF036708; AAB95404.1; -.
EMBL; AE016967; AAP56418.1; ALT_INIT.
HSSP; P02357; 1PKP.
                                                                                                                                                                                                                                                                                                                                                                           DRBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Binds DNA as a dimer. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AA; 24579 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 VVGDRKGRVGFGIAK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 LGAEAWGR---GVKK
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44
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SEQUENCE 255 AA; 29494 MW;
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                                                                                                                                                                                                                                                                                                                     27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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P54803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 VIVCPASVSSNEVSTT-ÉTAVHLCTETSKTSAVSVGAKDTHLÓPPÓKRRRPDVÍDSRNÍK 250
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"The chloroplast and mitochondrial genome sequences of the charophyte Chaetosphaeridium globosum: insights into the timing of the events that restructured organelle DNAs within the green algal lineage that led to land plants.",
Proc. Natl. Acad. Sci. U.S.A. 99:11275-11280(2002).
-! SUBUNIT: Part of the 30S ribosomal subunit.
-! SUBUNIT: Part of the 30S ribosomal subunit.
-! SUBCELLUAR LOCATION: Chloroplast.
-! SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-! SIMILARITY: Contains 1 KH type-2 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                      Early protein; Transcription regulation; Activator; DNA-binding;
Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 368 AA; 41739 MW; 3212B423B2F629D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Indels
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Chaetosphaeridiaceae, Chaetosphaeridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 27.0%; Pred. No. 15; les 24; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 YPNNLLRGQQSVDSTTRGLVTATECTNKG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGKGIVKGRNLDS -- RGLILGAEAWGRG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%; Score 65; 27.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LLVCEAIWRSNSGSNTLENGYFLSRN---
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InterPro; IPR009019; KH prok.
InterPro; IPR009019; KH TYPE 2.
InterPro; IPR001351; Ribosomal_S3_C.
InterPro; IPR008028; Ribosomal_S3_N.
InterPro; IPR008028; Ribosomal_S3_N.
Pfam; PP00189; Ribosomal_S3_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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MEDLINE=22177139; PubMed=12161560;
                                                                                                 HSSP; P17383; IDHM.
InterPro; IPR000427; E2_C.
InterPro; IPR001865; E2_N.
InterPro; IPR009021; Viral_DNA_bd.
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                                                                                                                                                                                                                                                                                             ProDom; PD000672; E2_C; 1. ProDom; PD000678; E2_N; 1.
                                        EMBL; X74481; CAA52588.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                             Pfam; PF00511; E2_C; 1.
Pfam; PF00508; E2_N; 1.
                                                            PIR; S36576; S36576.
HSSP; P17383; 1DHM.
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28-FEB-2003
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127 EKMWRYVQRSLTLSNGKFRMTLSKVSNPYKEANIVAEYIARQLENRVAFRRAMKQAIKDA 186
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MEDILINE=98084-2421, PubMed=9434135,
Sakai N., Fukushime H., Tani K., Fu L., Nishigaki T., Yanagihara I.,
Tatsumi N., Ozono K., Okada S.;
"Human palatacrocarebrosidase gene: promoter analysis of the 5'-flanking
region and structural organization."
Biochim. Biophys. Acta 1395:62-67(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
TISSUE-Placenta, and Skin fibroblast;
MEDLINE=94128088; PubMed=8297359;
Sakai N., Inui K., Fuji N., Fukushima H., Nishimoto J.,
Yanagihara I., Isegawa Y., Iwamatsu A., Okada S.;
"Krabbe disease: isolation and characterization of a full-length cDNA for human galactocerebrosidase.";
                                                                                                                                                                                                                                                                                                                                                                                              14 EAIWRSNSGSNTLENGYF---LSRNKENHSQPT----QSSLEDSVTPTKAVKTTGK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 27-59 AND 436-454. TISSUE-Brain, and Testis;
MEDIJNE=94108435; PubMed=8281145;
Chen Y.Q., Rafi M.A., de Gala G., Wenger D.A.;
"Cloning and expression of CDNA encoding human galactocerebrosidase, the enzyme deficient in globoid cell leukodystrophy.";
Hum. Mol. Genet. 2:1841-1845(1993).
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MEDLINE=95324938; PubMed=7601472;
Luzi P., Rafi M.A., Wenger D.A.;
"Structure and organization of the human galactocerebrosidage (GALC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Galactosidase precursor (BC 3.2.1.46) (GALCERase)
(Galactosylceramidase) (Galactosylceramide beta-galactosidase)
(Galactocerebroside beta-galactosidase).
Length 255;
                                                                                                                                                                                                  OABBCEE18062EAC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-45 AND 436-454, AND CHARACTERIZATION.
TISSUE=Urine;
MEDLINE=94002192; PubMed=8399327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 198:485-491(1994)
                                                                                                                                                                                                                                                                   Score 64; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 669 AA
                                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 KENGQVKGIKIQISGRINGAEIARVEWAR 215
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Hayashi K., Kobayashi T.;
"Adult onset globoid cell leukodystrophy (Krabbe disease): analysis of
galactosylceramidase cDNA from four Japanese patients.";
                                                                                                                                                                                                                                                                                                                                                        Rafi M.A., Luzi P., Chen Y.C., Wenger D.A.;
"A large deletion together with a point mutation in the GALC gene is a common mutant allele in patients with infantile Krabbe disease.";
Hum. Mol. Genet. 4:1285-1289(1995).
                                                                             MEDLINE=97478285; PubMed=9338580;
Wenger D.A., Rafi M.A., Luzi P.;
"Molecular genetics of Krabbe disease (globoid cell leukodystrophy):
diagnostic and clinical implications.";
Hum. Mutat. 10:268-279(1997).
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Furuya H., Kukita Y.-J., Nagano S., Sakai Y., Yamashita Y.,
Fukuyama H., Inatomi Y., Saito Y., Kolke R., Tsuji S., Fukumaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS GLD ARG-43; PHE-52; ILE-262; CYS-319; GLY-410; HIS-515 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96198195; PubMed=8786069; Rafi M.A., Luzi P., Zlotogora J., Wenger D.A.; "Two different mutations are responsible for Krabbe disease in the Druze and Moslem Arab populations in Israel."; Hum. Genet. 97:304-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS GLD HIS-63; SER-95; LEU-101; THR-234; SER-268 AND CYS-298,
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                                                                                                                                                                                                                         MEDLINE=20295342; PubMed=10833326;
Wenger D.A., Rafi M.A., Luzi P., Datto J., Costantino-Ceccarini
"Krabbe disease: genetic aspects and progress toward therapy.";
Mol. Genet. Metab. 70:1-9(2000).
"Galactocerebrosidase from human urine: purification and partial
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De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,
Raghavan S., Kolodny E.H.;
"Molecular basis of late-life globoid cell leukodystrophy.";
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MacFarlane H., Gusella J.F., Krivit W., Kolodny E.H.;
"Molecular heterogeneity of late-onset forms of globoid-cell
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MacFarlane H., Gusella J.F., Krivit W., Kolodny E.H.,
Am. J. Hum. Genet. 60:1264-1264(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96121583; PubMed-8595408;
Tatsumi N., Inui K., Sakai N., Fukushima H., Mishimoto J.,
Yanagihara I., Nishigaki T., Tsukamoto H., Fu L., Tanilke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS GLD ASP-270 AND ARG-537, AND VARIANT THR-625.
                                   Biochim. Biophys. Acta 1170:53-61(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular defects in Krabbe disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Hum. Genet. 59:1233-1242(1996).
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MEDLINE=99250870; PubMed=10234611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97094180; PubMed=8940268;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=96090246; PubMed=7581365;
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                     characterization."
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALSCELLANDOUS: Has an optimal pH between 4.0 and 4.4. Activity is lost when heated at 52 degrees Celsius for five minutes. SIMILARITY: Belongs to family 59 of glycosyl hydrolases. DATABASE: NAME=Genebis; NOTE=Krabbe disease; www="http://life2.tau.ac.il/Genebis/Tables/krabbe/krabbe.html".
                                                                                                                                                                                                          Isold=P54803-2; Sequence=VSP_001800, VSP_001801;
TISSUE SPECIFICITY: Highest level of activity in testes compared
to brain, kidney, placenta and liver. Can also be found in urine-
POLYMORPHISM: Polymorphic amino-acid changes are responsible for
the wide range of catalytic activities found in the general
                                                     galactosylceramide, galactosylsphingosine, lactosylceramide, and monogalactosyldiglyceride. Enzyme with very low activity responsible for the lysosomal catabolism of galactosylceramide, amajor lipid in myelin, kidney and epithelial cells of small intestine and colon. CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)O = D-galactoses + N-acylsphingosine.

ALTERNATIVE PRODUCES:
Nishigaki T., Tatsumi N., Tsukamoto H., Kokubu C.,
 Fu L., Inui K., Nishigaki T., Tatsumi N., Tsukamoto H. Muramatsu T., Okada S.; "Molecular heterogeneity of Krabbe disease."; "Inherit. Metab. Dis. 22:155-162(1999).
                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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Kitada K., Sugino A., Johnston L.H., Johnson A.L.,
"M multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
cycle mutant gene dbf4 encodes a protein kinase and is identified as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97313268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G., "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21264235; PubMed-11371343; Meckuller K., Poupart M.-A., Nasmyth K.; Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 Kinase regulates sister chromatid separation in yeast."; Cell 105:459-472(2001).
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Phosphorylates SCC1/MCD1.
-I- CATALYTIC ACTIVITY ATP + a protein = ADP + a phosphoprotein.
-I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
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10-OCT-2003 (Rel. 42, Last amnotation update)
10-OCT-2010 (Rel. 42, Last amnotation update)
10-OCT-2010 (Rel. 42, Last amnotation update)
10-OCT-2013 (Rel. 42, Last amnotation update)
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-!- SIMILARITY: Contains 2 POLO box domains.
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                                                                                                                                                       13.7%; Score 63.5; D 23.5%; Pred. No. 43; ive 15; Mismatches
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D86181; BAA24902.1; -. B4232; BAA24902.1; JOINED. D84233; BAA24902.1; JOINED. D84234; BAA24902.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION OF SCC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDC5 YE?
P32562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDC5_YEAST
                                                                                              EMBL;
                                 EMBL;
                                                               EMBL;
                                                                                                                                                                                                                          Matches
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   R R R R
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van der Aart Q.J.M., Kleine K., Steensma H.Y.; "Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SMI1-PH081-YHB4-PFK1 region from the right arm of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Philips J., Herskowitz I.;
"Identification of Kellp, a kelch domain-containing protein involved
in cell fusion and morphology in Saccharomyces cerevisiae.";
J. Cell Biol. 143:375-389(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                    R Germolline; latebes; ...

R GO; GO:0005935; C:bud neck; IDA.

R GO; GO:0005234; C:bud neck; IDA.

R GO; GO:000522; C:spindle pole; IDA.

R GO; GO:0006261; P:DNA dependent DNA replication; IDA.

R GO; GO:0006268; P:protein amino acid phosphorylation; IDA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IDA.

R InterPro; IPR00039; POUC_box.

R InterPro; IPR00219; Pouc_kinase.

R InterPro; IPR00229; Ser_thr_pkinase.

R InterPro; IPR00259; Pouc_box; 2.

R Pfam; PR0069; pkinase; 1.

R Pfam; PR0069; pkinase; 1.

R Pfam; PR0069; Prot_kinase; 1.

R PROSITE; PS00109; TrxKINASE; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R RROSITE; PS00101; PROTEIN KINASE BOX; 1.

R ROSITE; PS00101; PROTEIN KINASE ST; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

R Transferase; ATP-binding; Repeat.

R Transferase; ATP-binding; Repeat.

R Transferase; ATP-binding; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 LSRNKENHSQPTQSSLEDSV-----TPTKAVKTTGKGIVKGRNLDSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDPNNDHHHQPAQKKKRBEKLSALCKTPPSLIKTRGKDYHRGHFLGEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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ATP (BY SIMILARITY)
BY SIMILARITY.
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
16-0CT-2003 (Rel. 42, Last annotation update)
KELL PEPRATS Protein 2.
KELL OR YGR238C OR G88585.
Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81030 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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PIR; A48144; A48144.
HSSP; Q63450; 1A06.
GermOnline; 142669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 AA;
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61 GKGIVKGRNLDSRGLILGA--EAWG
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Pfam; PF00215; OMPdecase; 1.
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                                                                                                                                                                                                                                                                                                                                                            13.6%;
                                                                                                                                                                                                                                                                                                                              8817 MW;
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 27.1%;
les 23; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                        43
77
80
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                                                                                                                                                                                                                                                                                                                                 80 AA;
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46
79
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PEPTIDE
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MOD_RES
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IMCESLHAGESFSNSLSGGFTPSKSTESENQEIINILTPRLPDSKVLSYNDIDEGAGSYS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --0 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of cDNAs encoding new peptides of the dermaseptin-family.";
Biochim. Biophys. Acta 1388:279-283(1998).
-!- FUNCTION: Possesses a potent antimicrobial activity against Grampositive and Gram-negative bacteria. Probably acts by disturbing membrane functions with its amphipathic structure (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLEDSVTPTKA-------VKTTGKGI-VKGRNLD-SRGLILGAEAWGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dermaseptin AA-3-6 precursor.
Agalychnis annae (Yellow-eye leaf frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                      GO; GO:0005935; C:bud neck; IDA.
GO; GO:0005934; C:bud tip; IDA.
GO; GO:0005937; C:shmoo tip; IDA.
GO; GO:0000747; P:conjugation with cellular fusion; IGI.
InterPro; IPR006652; Kelch_rep.
Pfam; PF01344; Kelch; 4.
Kelch_repeat; Repeat; Coiled coil.
            -!- SIMILARITY: Contains 4 Kelch repeats.
-!- SIMILARITY: TO YEAST KEL! AND S.POMBE SPACGG10.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                  63B9772FF017E6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LVCEAIWRSNSGSNTLENGYFLSRNKENHSQPT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 63.5; 20.8%; Pred. No. 59
                                                                                                                                                                                                                                                                                                                             ; Coiled coil.

KELCH 1.

67 KELCH 2.

17 KELCH 3.

69 KELCH 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin;
MEDLINE=98449786; PubMed=9774745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  99974 MW;
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                                                                                                                                                                      EMBL; X87941; CAA61189.1; -.
                                                                                                                                                                                    EMBL; Z73023; CAA97266.1; -. PIR; SS7704, SS7704, SS7704, GermOnline; 141550; -. SGD; S0003470; KEL2.
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369
685
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550
728
882 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 VKKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cretidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
(OMPDCase) (OMPdecase) (Uridine 5'-monophosphate synthase) (UMP
SIMILARITY: Belongs to the frog skin active peptide (FSAP) family. Dermaseptin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIFFLSLLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTGSSLEDSVTPTKAVKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-78 PROVIDE AMIDE GROUP)
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Pachysolen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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Submitted (FBB-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UNP + CO(2).
--- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
--- SIMILARITY: Belongs to the OMP decarboxylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 63; DB 1; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Indels
                                                                                                                                                                                                                                                                                                                DB13FD831E7E2140 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DERMASEPTIN AA-3-6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LVLFLGLVSLSICEEEKREN-------
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POL OR MJ0885.
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                     SEQUENCE
                                                            Query Match
Best Local S
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                                                                                                                                                2
                                                                                                                                                                                                                               -----KIAQWADITNAHGVIGEGIVKGLKEAALETILEP 146
                                                                                                                                                                                      20 NSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKGIVKG-----RNLDS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane; Repeat; CBS domain; Complete proteome.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium Spreachocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
-!- CCFATTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 2 CBS domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8530279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBS 1.
ZINS 2.
ZINC (CATALVTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                         Length 268;
                                                                                                                                                Indels
                                             Y SIMILARITY.
ECC89602DA2FC10A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                23;
                                                                                                         62.5; DB 1;
PROSITE; PS00156; OMPDECASE; 1.
Pyrimidine biosynthesis; Lyase; Decarboxylase.
ACT SITE
95 95
BY SIMILARITY
95 97
2000RDE 268 AA; 29684 MW; ECC89602DA2FC10)
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein sll0528 (EC 3.4.24.-).
5LL0528.
                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      379 AA
                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, D64006, BAA10876.1; -.
PIR, S76029, S76029.
MEROPS, M50.UPB, -.
InterPro; IPR006644; CBS domain.
InterPro; IPR006045; Pept M Zn BS.
InterPro; IPR008915; Peptidase_M50.
Pfam; PF00163; Peptidase_M50.
Pfam; PF00163; Peptidase_M50; I.
Pfam; PF00163; Peptidase_M50; I.
PROSITE; S001042; ZINC PROTEASE; I.
Hypothetical protein; Hydrolase; Metal
                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803)
                                                                                                           Score
                                                                                                       13.5%;
28.8%;
                                                                                                                                                                                                                                                                                                  |||:: ||
147 RGLLMLAELSSKG 159
                                                                                                                                                                                                                                                                          85
                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
168
232
310
                                                                                                                                                                                                                                                                          73 RGLILGAEAWGRG
                                                                                                                                                                                                                                 101 NTVKNOYKNGIF-
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SYNYS
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DOMAIN
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                      Y528 SY
Q55518;
                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
Y528_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                      THE TETETER WAS BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH 
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                      211 LGILNILPIGSFWTILIGWFLLQNAGSSARNAQVKEQMEAFTAEDAVIPNSPIIPAGLNI 270
                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 273:1058-1073(1996).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ { DNA} (N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECURNCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8680807;

MEDLINE=96337999; PubMed=86808087;

Bull C.J., White O., Olsen G.J., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Kerlavage A.R., Meinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghaen N.S.M., Weidman J.F., Puhrmann J.L., Ngnyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordouvsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PTM: This protein undergoes a protein self splicing that involves a post-translational excision of the intervening region (intein) followed by peptide ligation (Potential).
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                       5 LSLILLLVCBAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKGI
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
                                                                                                                                                         7;
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                          Length 379;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococus.
                           1CC3251660078ECB CRC64;
                                                                                                 DB 1;
                                                                                       %; Score 62.5; DE
%; Pred. No. 29;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1634 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR006172; DNA_pol_B.
Interpro; IPR006134; DNA_pol_B dom.
Interpro; IPR006133; DNA_pol_B exo.
Interpro; IPR0051587; Hedgehog_hint_N
Interpro; IPR003586; Hedgehog_hint_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPRO066142; INTEIN.—
Interpro; IPRO06042; Intein endonuc.
Interpro; IPRO0641; Intein_S.
Interpro; IPRO06478; Pol2.
Pfam; PF00136; DNA_pol_B; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                65 -----VKGRNLDSRGLILGAE 80
                                  40465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67532; AAB98889.1; -.
                                                                                                 13.5%;
26.5%;
                                                                                                                                                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P56689; 1TGO.
TIGR; MJ0885; -
                                      379 AA;
                                                                                                                                    Similarity
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEF2A OR SL2
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                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99310339; PubMed=10382966;

Rawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,

Rawarabayasi Y., Hino Y., Horikawa H., Raba S.-I., Ankai A., Kosugi H.,

Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,

A desoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,

A akamiya M., Masuda S., Punahashi T., Tanaka T., Kudoh Y.,

Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kudoh Y.,

Nakamura Y., Nomura N., Sako Y., Kikuchi H.;

Nomura Y., Nomura N., Sako Y., Kikuchi H.;

Nomplete genome sequence of an aerobic hyper-thermophilic

Tronglete genome sequence of an aerobic hyper-thermophilic

I. PUNCINION: Dimethylate Sadenosyl-L-methionine as donor of the

methyl groups (By similarity)

C. - CAPALITIT (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIT (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIT (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: Sadenosyl-L-methionine + ENNA = S-adenosyl-L-

C. - CAPALITIC (ATIVITY: S
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                                                                                                                                                                                                                                                                                                                                                                                                                      ---PTKAVKTTGKGIVKGRNLDSRGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N(2),N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32)
(tRNA(quanine-26,N(2)-N(2)) methyltransferase) (tRNA 2,2-
dimethylguanosine-26 methyltransferase)
(tRNA(m(2,2)236)dimethyltransferase).
TRMI OR APE0782.
Length 1634;
                                                                                                                                                                                                                                                         MJA POL-1 INTEIN (POTENTIAL).
POL, 2ND PART (POTENTIAL).
MJA POL-2 INTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archãéa; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                          POL, 3RD PART (POTENTIAL).
IN; 84AIFAFABIF97DDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homocysteine + tRNA containing N(2)-methylguanine. SIMILARITY: Belongs to the TRM1 family.
                                                                                                                                                                                                  Transferase; DNA-directed DNA polymerase; DNA replicat:
DNA-binding; Autocatalytic cleavage; Protein splicing;
                                                                                                                                                                                                                                             1ST PART (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 1; I
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        25 TLENGYFLSRNKENHSOPTOSSLEDSVT----
                                                                                                                                                                                                                                                                                                                                                            Score 62;
                                                                                                                                                                                                                                                                                                                                                                                        .,6
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NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                            13.4%;
                                                                                                                                                                                                                                                                                                                               191708
                                                                                                                                                                                                                                                                                                                                                                           29.28;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.2%
Matches 21, Conservative
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453 LGIDGWQK-VKK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 LGAEAWGRGVKK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                               425
794
882
1358
                                                                                                                                                                                                                                                            426 79
795 88
883 135
1359 163
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                                                                                                                                                                                                                                   Complete proteome.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 NARANGLEPGSYMIFNKESNSLMFHLSRERPTPVSLIDIDPYGSPAPFVDAALALSGKGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 NSGSNTLENGYFLSRNKENHS-----QPTQSSLED----SVTP--TKAVKTTGKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBRYO AND MAY REGULATE MUSCLE-SPECIFIC TRANSCRIPTION IN THE EMBRYO AND MAY REGULATE MUSCLE-SPECIFIC TRANSCRIPTION OF A VARIETY OF CELL TYPES IN THE ADULT. IT BINDS TO THE SEQUENCE CTA(T/A) ATAR.

-1 SUBCELLULAR LOCATION: Nuclear.

-1 TISSUE SPECIFICITY: RESTRICTED TO THE SOMITIC MESODERM OF EARLY EMBRYOS AND TO THE BODY MUSCLE (MYOTOMES) OF THE TADFOLE.

EXPRESSED IN ALL TISSUES EXAMINED IN THE ADULT.

-1 DEVELOPMENTAL STAGES EXAMINED IN THE ADULT.

-1 SIMILARITY: Belongs to the MEP2 family.

-1 SIMILARITY: Contains 1 MADS-box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93099873, PubMed=1281451;
Chambers A.E., Kotecha S., Towers N., Mohun T.J.;
"Muscle-specific expression of SRF-related genes in the early embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myocyte-specific enhancer factor 2A homolog (Serum response factor-
like protein 2) (SL-2).
                                                                                                                                                                                                                                                                                                                                                                     Transferase, Methyltransferase, tRNA processing, Complete proteome. SEQUENCE 401 AA; 43034 MW; 570005B39E83366E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.3%; Score 61.5; Dl
29.9%; Pred. No. 40;
iive 12; Mismatches
                                                                                                                                                                                                         EMBL; AP000060; BAA79760.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 VVAMTATDLAVLEGGKA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                   HAMAP; MF 00290; -; 1.
InterPro; IRR002905; TRM.
Pfam; PF02005; TRM; 1.
TIGRFAMS; TIGR00308; TRMI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, Z19123, CAA79530.1, -.
PIR, S28060, S28060.
HSSP, P11831, 1SRS.
TRANSFAC, T01784; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11:4981-4991 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKGRNLDSRGLILGAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similari,
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Xenopus laevis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XMX6 YE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
YMX6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 NGAGTSPVGNGFVNPRASPSHLGPTGGNVLGKVMPTKSPPPPGGNLVMNSRKPDLRVVI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKGIV-KGRNLDSRGLI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21881936; PubMed=11884590;
Ohi M.D., Link A.J., Ren L., Jennings J.L., McDonald W.H., Gould K.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                               Transcription regulation; Muclear protein; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 61.5; DB 1; Length 516; 28.8%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                         8C855505AC123F4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPPER 9: 074221;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cell cycle control protein cwf22.
CWF22 OR SPBCI3E7.01 OR SPBCI5D4.16.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                                        MADS-box.
MEF2-TYPE (POTENTIAL).
ARG/LYS-RICH (BASIC).
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 53;
12; Mismatches
                                                                                                                                                                                                                                                                                                        GLN/HIS-RICH.
SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21848401; PubMed=11859360;
                                                                                                        PROSITE; PS00350; MADS BOX 1; 1.
PROSITE; PS50066; MADS BOX 2; 1.
          IPR002100; TF MADSbox.
                                                                                                                                                                                                                                                                                                                                                            56403 MW;
             Interbro; IPR002100; TF_MADSb
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                   SMART; SM00432; MADS; 1
                                                                                                                                                                                                                               86
31
225
460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                            516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                        Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION.
                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHPO
                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                  DNA BIND
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CWFM_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . .; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 SSSYSSTYSRGRSYSRSTSYSKSRSYSRSYTPINNINHK-KYIRKDRELSPRG 685
"Proteomics analysis reveals stable multiprotein complexes in both fission and budding yeasts containing Myb-related Cdc5p/Ceflp, novel pre-mRNA splicing factors, and snRNAs."; Mol. Cell. Biol. 22:2011-2034 (2002).
-: FUNCTION: Involved in mRNA splicing where it associates with cdc5 and the other cwf proteins as part of the spliceosome.
-: SUBUNIT: Interacts with cdc5.
-: SUBCELULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKGIVKGRNLDSRG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=S2886 / AB972;
MEDLINE=97313268; PubMed=9169872;
MEDLINE=97313268; PubMed=9169872;
MEDLINE=97313268; PubMed=9169872;
Connor R., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Tice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 105.9 kDa protein in ADH3-RCA1 intergenic region.
YMR086W OR YM9582.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61.5; DB 1; Length 8 Pred. No. 91; 7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; mRNA processing; mRNA splicing.
SEQUENCE 834 AA; 96378 MW; 25EDAE85E19F3FB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         960 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: SOME, TO YEAST YKL105C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL031349; CAA20491.1; -.
EMBL; AL354632; CAB89876.1; -.
GeneDB SPowbe; SPBC13E7.01; -.
GO; GO:0005554; C:uccleoplasm; ISS.
GO; GO:0006397; P:uccleoplasm; ISS.
GO; GO:0006371; P:uccleoplasm; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPPR008938; ARM
Interpro; IPR008903 IF eIF4G.
Interpro; IPR003891; IF eIF4G_MA3.
Pfam; PF02847; MA3; 1.
SMART; SM00544; MA3; 1.
SWART; SM00544; MA3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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3;
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                          Query Match
Best Local Similarity 36.2%; Pred. No. 1.18+02;
Matches 21; Conservative 10; Mismatches 20; Indels
                                                             EMBL; Z49259; CAA89232.1; -.
PIK; S54461; S54461.
GermConline; 142754; -.
SGD; S0004692; YMR086W.
Hypothetical protein.
SEQUENCE 960 AA; 105873 MW; 05A4FA27129DB09B CRC64;
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Search completed: March 31, 2004, 12:14:02 Job time : 15 secs

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GenCore version 5.1.6
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protein search, using sw model ī OM protein March 31, 2004, 12:11:36; Search time 20 Seconds (without alignments) 432.862 Million cell updates/sec Run on:

US-09-989-293A-377 Title:

462 1 MTFFLSLILLLLVCEAIWRSN......DSRGLILGAEAWGRGVKKNT 90 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	anti-rep	н	(h	rhol_gdp-gtp excha	_	8	hypothetical prote	pti	protein distantly	in -	а.	hypothetical prote	0		щ	site-specific DNA-	unknown protein F9	galactosylceramida	protein kinase CDC	S-receptor kinase	chetical prot	repressor	anti repressor [im	hypothetical prote		surface layer prot	Н,	hypothetical prote
Ω	AE1734	р д 6 4	90		02	0	49	₩	H97313	836576	T24654	T06029	AI1442	T46099	391	A64594	A96781	154205	A48144	T14472	S57704	T00169	8998	F86185	657	D69426	876029	T19402
	01 C	40	1 (1	7	7	Н	~	~	7	7	7	N	7	7	N	7	7	7	0	7	7	~	7	7	C)	7	N	7
ength	256	4 7 7 7 7 7	280	1334	337	479	851	313	360	368	379	532	257	430	548	598	651	699	705	850	882	249	250	441	457	2425	379	381
% Query Match	15.2	* 4	14.7	4.	14.4	4.	14.3		14.1	14.1	14.1	•		13.9	•	13.7	13.7	13.7	13.7	ε,	13.7	ω,	m.	ъ.	13.6	ω.	ω,	ω.
Score	700	0.00 0.00	. 6	68	9	66.5	99	65	65	65	65	64.5	64	64	64	63.5	•	ω.	63.5	<u>ر</u>	63.5	63	63	63	63	63	•	CI.
	 H (7 6	J 4	. rv	φ	7	89	6	10	디	12	13	14	15	16	17	7.8	19	20	21	22	23	24	25	26	27	28	29

conserved hypothet	hypothetical prote	S-receptor kinase	hypothetical prote	hypothetical prote	probable lipoprote	hypothetical profe	protein C45G9.6 [i	major surface glyc	major surface glyc	DNA-directed DNA p	probable N2,N2-dim	cellulase (EC 3.2.	serum response fac	hypothetical prote	conserved hypothet
AF2897	H97672	S51527	AD2045	T18502	F81128.	876835	A88448	T30542	T30543	E64410	H72669	S22458	528060	C96501	T39492
~	~	Н	0	~	2	2	~	7	~	7	~	(7	~	~	0
617	641	849	1123	1553	84	149	613	1017	1022	1634	409	500	516	668	887
13.5	13.5	13.5	13.5	13.5	13.4	13.4	13.4	13.4	13.4	13.4	13.3	13.3	13.3	13.3	13.3
62.5	62.5	62.5	62.5	62.5	62	62	62	62	62	62	61.5	61.5	61.5	61.5	61.5

ALIGNMENTS

Н	
Н	4
ᆸ	7
ĕ	r

(strain Clip11262) RESULT 1 AE1734 anti-repressor homolog lin2418 [imported] - Listeria innocua

Cispecies: Listeria innocua
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Cipates: P: Frangeul, L: Buchrieser, C:; Amend, A:; Baquero, F:; Berche, P:; Bloec.
D:; Dominguez-Bernal, G:; Duchaud, B:; Durand, L:; Dussurget, O:; Entian, K.D.; Fsihi, D:; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J: Kuhn, M: Kunst, F:; Kurapkat, G:; Madueno, B:; Maitournam, A.; A;Atitle: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AE1734 A; Status: preliminary

A;Molecule type: DNA A;Residues: 1-256 «GLA» A;Cross-references: GB:AL592022; PIDN:CAC97645.1; PID:g16414940; GSPDB:GN00178 A;Experimental source: strain Clip11262 C;Genetics:

A; Gene: lin2418

Gaps 14; Length 256; Indels 13; Query Match
15.2%; Score 70; DB 2;
Best Local Similarity 31.4%; Pred. No. 5.6;
Matches 16; Conservative 8; Mismatches 1:

Η;

--AVKTTGKG 63 27 ENGYFLSRNKENHSQPTQSSLEDSVTPTK-g à

RESULT 2

hypothetical protein - Synechocystis sp. (strain PCC 6803)
hypothetical protein - Synechocystis sp.
C;Species: Synechocystis sp.
A;Variety PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76967
E;Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

A.Reference number: S74322; MUID:97061201; PMID:8905231
A,Accession: S76967
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-495 «KAMs
A,Residues: 1-495 «KAMs
A,Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10659.1; PID:d101
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE004091; NID:g9951241; PIDN:AAG08351.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-1334 <NOO>
A,Cross-references: EMBL:AL049498; PIDN:CAB39903.1; GSPDB:GN00068; SPDB:SPCC645.07
A,Experimental source: strain 972h-; cosmid c645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PA4966 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Species: Dsequence revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83026
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, S; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, J. Lolson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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--KMAPAVSPNKTIEGLVGGIV-- 196
                                                                                                                                                                                           rhol gdp-gtp exchange protein 1 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 23-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 WRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKGIVKGRNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 894/3
C;Superfamily: GDP/GTP exchange protein ROM1; CDC24 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AIWRSNSGSNTLENGYFLSRNKENHSOPTOSSLEDSVTPT---
                                                                                                                                                                                                                                                                         C,Accession: T41524
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z22000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%; Score 66.5; DB 2; 25.7%; Pred. No. 18; ive 12; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%; Score 68; DB 2;
21.8%; Pred. No. 59;
:ive 19; Mismatches 2;
151 LVLFVCFLVWAADSGA-----YFVGKSLGKH---
                                                                                      210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                              83
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A,Molecule type: DWA
A,Residues: 1-37 < STO>
A,Gross-references: GB:AB004909; GF
A,Experimental source: strain PAO1
                                                                           :::| |::|
----TAMLVGYWVAECFG
                                              68 RNLDSRGLILG---AEAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 RGGNLDFEGIACDA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 KGRNLDSRGLILGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: SPDB:SPCC645.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: PA4966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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S41015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-280 <HEI>
A;Cross-references: GB:AE004297; GB:AE003852; NID:g9656810; PIDN:AAF95399.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                        transferrin receptor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C;Accession: A34549
R;Roberts, K.P.; Griswold, M.D.
A01. Endocrinol. 4, 531-542, 1990
A;Fitle: Characterization of rat transferrin receptor CDNA: the regulation of transferrin A;Reference number: A34549; MUID:91125359; PMID:2126342
A;Accession: A34549
A;Status: preliminary
A;Residues: 1-622 <ROB:
A;Residues: 1-622 <ROB:
A;Residues: 1-622 <ROB:
A;Crooss-references: GB:M58040; NID:g207463; PIDN:AAA42273.1; PID:g207464
C;Superfamily: transferrin receptor
C;Keywords: receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A,Reference number: A82035, WUID:20406833, PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                   2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                             ---NHSQPTQSSLEDSVTPTKAVKTTG-KGIVKGRNLD 71
                                                                                                                         ----GIVKGRNLDSRGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 622;
         Length 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                   Indels
                                                   26;
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           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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C;Superfamily: phosphatidate cytidylyltransferase
       Score 68.5; DE Pred. No. 17; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 68.5; D
llarity 27.6%; Pred. No. 22;
Conservative 15; Mismatches
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VGAORDAWGPGVAKSS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGA--EAWGRGVKKNT 90
         Query Match
Best Local Similarity 32.3%;
Matches 20; Conservative
                                                                                                    21 SGSNTLENGYFLSRNKE-
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ses 21; Conserv
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A, Molecule type: DNA
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                                                                                                                                                                                         SR 73
                                                                                                                                                                                                                                   LR 84
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Best Local S
Matches 20
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Best Local S:
Matches 21
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M.J., K., L

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protein distantly similar to N-terminal truncated of HSP60 chaperonin family [importer c; Species: Clostridium acetobutylicum C; Species: Lq.Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: H97313 R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                           RiHeidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R., chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
                             transcription regulator LysR family VCA0635 [imported] - Vibrio cholerae (strain N169 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: A62436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-313 <HEL>
A;Residues: GB:AE004393; GB:AE003853; NID:g9658042; PIDN:AAF96536.1; GSPDB:GN
A;Experimental source: serogroup 01; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-360 <KUR>
A;Residues: 1-360 <KUR>
A;Cross-references: GB:AB001437; PIDN:AAK81299.1; PID:g15026451; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: 836576
R;Deflus, H; Hofmann, B
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT-----GKGIVKGRNLDSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 SNTLENGYFLSRNKENHS---OPTOSSLEDSVTPTKAVKTTGKGIVKGRNLD-SRGLILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%; Score 65; DB 2; Length 360; llarity 29.3%; Pred. No. 28; Conservative 18; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 2
C,Superfamily: conserved hypothetical protein HI1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 2;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%;
38.3%;
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es 22; Conserv
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Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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A;Gene: VCA0635
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Matches
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transcription factor tbx8 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R; Berks, M.
submitted to the EMBL Data Library, January 1994
A; Reference number: S41014
A; Reference number: S41014
A; Residues: 1479 < BER>
A; Residues: 1479 < BER>
A; Residues: 1479 < BER>
A; Residues: 1479 < BER>
A; Residues: 1479 < BER>
A; Residues: 129, 1995
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A; Residues: 130, 1995
A; Residues: 130, 1995
A; Cross-references
A; Introns: 77/3; 101/3; 134/3; 236/2; 261/3; 312/3; 450/3
C; Superfamily: Caenorhabditis elegans transcription factor tbx8; T-box homology
C; Reywords: DNA binding
F; 153-340/Domain; T-box homology < TEX>
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: ||| : |:| || 85 AHGASNT-----NKINQNLSRP-HPAKGHRKTIPTSVIATVPRGPPSGR-
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14.4%; Score 66.5; DE
Best Local Similarity 25.0%; Pred. No. 27;
Matches 18; Conservative 13; Mismatches
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Pred. No.
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25.6%;
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-QEWGRGIQRKT 137
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Best Local Similarity
Matches 20; Conserv
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A; Note: F9K21.130
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Length 313;

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RESULT 9

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C;Species: Listeria innocua cavision 27-Nov-2001 #text_change 27-Nov-2001 C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: Al1442
C;Accession: Al1442
C;Accession: Al1442
C;Accession: Al1442
C;Accession: District C; Amend, A.; Baquero, F.; Berche, P.; Bloed)
C; Dominguez-Bernal, G; Duchaud, E.; Durand, D.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Authors: Comparative genomics of Listeria species. Boland, J.A.; Voss, H.; Wehlan A;Reference number: AB1077; MUID:21837279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T25B15.60 - Arabidopsis thaliana ($\text{C}$)$pecies: Arabidopsis thaliana ($\text{mouse-ear}$ cress)
C;\text{Species: Arabidopsis thaliana ($\text{mouse-ear}$ cress)
C;\text{Data}$ cossion: T46090
R;\text{Alcaraz}, \text{J}.P; Clabault, \text{G}.; \text{Cottet}, \text{A}.; \text{Mache}, \text{R}.; \text{Mewes}, \text{H.W.}; \text{Lemcke}, \text{K}.; \text{Mayer}, \text{A};\text{Reference number: } \text{Z3021}
A;\text{Accession: } \text{T46099}
                                                                                                                                                      anti-repressor (Bacteriophage A118) homolog lin0080 [imported] - Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95313.1; PID:g16412500; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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C;Superfamily: Arabidopsis thaliana hypothetical protein T16L24.240
                          || :||
-----KVKESGK 317
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14 EAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL132972
A;Experimental source: cultivar Columbia; BAC clone T25B15
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                          Match 13.9%; Score 64; DB 2; Local Similarity 27.4%; Pred. No. 45; es 20; Conservative 14; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 2;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 25;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 ENGYFLSRNKENHSQPTQSSLEDSVTPTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 31, 2004, 12:15:28 Job time : 22 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 3
A,Introns: 23/3; 122/3; 194/3; 234/3
A,Note: T25B15.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 WRSNS--GSNT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 13.9%;
1 Similarity 29.4%;
15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-430 <ALC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: lin0080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                              274
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Sacession: T66029
R.Sevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bebvan, M.; Ven Protein Sequence Database, March 1999
A.Reference number: Z15484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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A;Reference number: Z19918

A;Accession: T24654

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-379 <WIL>
A;Cross-references: EMBL:Z81588; PIDN:CAB04712.1; GSPDB:GN00019; CESP:T07D10.2

A;Experimental source: clone T07D10

C;Genetics: A;Gene: CESP:T07D10.2
                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T24654
R;White, S.
                     A;Accession: 836576
A;Molecule type: DNA
A;Residues: 1-368 < CEL-
A;Cross-references: EMBL:X74481; NID:g397038; PIDN:CAA52588.1; PID:g397042
C;Superfamily: papillomavirus E2 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                  - KENHSQPTQSSLEDSVTPTKAVK
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A;Cross-references: EMBL:AL035709; GSPDB:GN00062; ATSP:T28I19.100
A;Cross-references: cultivar Columbia; BAC clone T28I19
C;Genetics:
A;Gene: ATSP:T28I19.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 532;
                                                                                                                                                                                           Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Indels
                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYLCVCKAVWKSTSFSSSLRN----NMKKMEHMKLTEKN 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T07D10.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSS
                                                                                                                                                                                      Query Match
14.1%; Score 65; DB 2;
Best Local Similarity 27.0%; Pred. No. 29;
Matches 24; Conservative 11; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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Pred. No. 50;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     251 YPNNLLRGQQSVDSTTRGLVTATECTNKG 279
                                                                                                                                                                                                                                                                                                                                                                            59 TTGKGIVKGRNLDS--RGLILGAEAWGRG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65;
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Map position: 1
A;Introns: 37/3; 85/3; 271/1; 319/1
C;Superfamily: oxytocin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%;
34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.9%;
Matches 14; Conservative
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Best Local Similarity 34.7'
Matches 17; Conservative
       A, Reference number: S36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-532 <BEV>
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein March 31, 2004, 12:12:31; Search time 23 Seconds (without alignments) 202:015 Million cell updates/sec Run on:

US-09-989-293A-377 Title: Perfect score:

462 1 MTFFLSLLLLLVCEAIWRSN.....DSRGLILGAEAWGRGVKKNT 90 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched: 389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

1. /ognZ_6/ptodata/2/iaa/5A_COMB.pep:*

2. /ognZ_6/ptodata/2/iaa/6A_COMB.pep:*

3. /ognZ_6/ptodata/2/iaa/6A_COMB.pep:*

4. /ognZ_6/ptodata/2/iaa/AB_COMB.pep:*

5. /ognZ_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6. /ognZ_6/ptodata/2/iaa/PorTUS_COMB.pep:*

6. /ognZ_6/ptodata/2/iaa/PorTUS_COMB.pep:*

6. /ognZ_6/ptodata/2/iaa/PorTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		o				
Result No.	Score	Query Match	Length	DB	ID	Description
	143.5	31.1	244	3	US-08-772-440-2	Sequence 2, Appli
(3)	139.5		50	m	US-08-772-440-25	25,
8	139.5		176	m	US-08-772-440-8	
4	128.5		180	m	-08-	37
ហ	69.5	15.0	171	4	US-09-205-258-481	48
9	69.5	រ	257	4	9-205-258-42	42
7	ω	14.8	622	٦	US-08-547-197-1	7,
80	68.5	14.8	622	m	US-08-957-940-1	Sequence 1, Appli
σn	9	4	354	4	US-09-252-991A-32891	32891,
10		14.2	247	4	US-09-134-000C-6345	
11	65	4.	461	4	US-09-134-001C-3604	3604,
12	64	m	126	4	US-09-198-452A-1254	
13		13.7	317	4	US-09-594-506-30	30, AF
14	63.5	13.7	881	4	US-09-489-039A-12003	
15	63	13.6	315	4	US-09-134-001C-4255	4255
16	62	13.4	1017	4	US-09-762-724-12	
17	62	13.4	7	4	US-09-762-724-14	14,
18	62	13.4		4	US-09-762-724-8	Seguence 8, Appli
19	61.5	13.3		m	US-08-960-780-6	ý
20	61.5			ጣ	t	
21	61.5	13.3		4	US-09-002-285-90	90,
22			78	4	US-09-589-477-90	Sequence 90, Appl
23	61.5		7	4	US-09-850-351A-6	ģ
24	61	13.2	23	'n	US-08-808-148-3	Sequence 3, Appli
25	61		C)	4	-594-	21
26	61	٠	254	4	-09-252-9	21
27	9	13.0	7	4	US-09-107-532A-6400	64

		Sequence 5734, Ap	Sequence 31892, A		Sequence 10, Appl	Sequence 4, Appli	7	ν,	æ	7	ci.	Sequence 6, Appli	9	Sequence 6, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 6, Appli
US-09-762-724-6	US-09-252-991A-26577	US-09-543-681A-5734	US-09-252-991A-31892	US-08-836-567-10	US-09-606-304-10	US-09-386-962C-4	US-09-341-461-2	US-09-030-267-5	US-08-619-812-8	US-07-908-253-2	US-08-455-970A-2	US-08-387-156-6	US-08-694-865-6	US-08-878-748-6	US-08-535-837-2	US-09-124-491-6	US-09-383-912-6
4	4	4	4	m	4	4	4	ო	m	Н	Н	Н	~	7	N	٣	4
1029	237	921	415	641	641	1742	3623	418	924	976	926	926	926	926	926	926	926
3.0	6.5	5.9	8.7	8.	12.8	2.8	2.8	2.7	2.7	12.7	12.7	2.7	12.7	12.7	12.7	2.7	2.7
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9	σ	59.5	50	50		59	59	58.5	58.5	58.5	58.5	58.5		58.5	58.5	58.5	58.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 2, Application US/08772440

Batent No. 6046158

GENERAL INFORMATION:
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BN PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: BARKET, David L.
REGISTRATION NUMBER: 32,165
REBERENCE/DOCKET NUMBER: 32,165
REBERENCE/DOCKET NUMBER: 32,165
RELEFRA: 512/418-300
TELLEFRA: 512/418-300
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                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston STATE: Texas COUNTRY: USA ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 244 amino acids
amino acid
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Best Local Similarity
Matches 29; Conserv
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TOPOLOGY: linear
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Sequence 8, Application US/08772440

Sequence 8, Application US/08772440

Patent No. 6046158

PAPLICANT: Takabilina, Akira

APPLICANT: Takabilina, Akira

TITLE OF INVENTION: UNIQUE DENDRIFIC CELL-ASSOCIATED C-TYPE

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
              Sequence 25, Application US/08772440

Sequence 25, Application US/08772440

Septent No. 6046158

GENERAL INFORMATION:
APPLICANT: Ariazumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 WRHNSGRNPEEKDNFLSRNKENH-KPTESSLDEKVAPSKASQTTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 139.5; DB 3; Length
Pred. No. 2.6e-10;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 WRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTG 61
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILLING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Parker, David L.
REGISTATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPRORE: 512/474-7577
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
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COUNTRY: USA
77210
                                                                                                                                                                                                                                                                                                  STATE: Texas
COUNTRY: USA
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RESULT 2
US-08-772-440-25
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SOUTHING STEER, PLOSING-DOS
TELEMENT APPLICATION UNITS
ATTORNAY/GRATH INPORVATION:
ATTORNAY/GRATH INPORVATION:
TELEMENT STEER, DAY 0.1
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DB 3; Length 180;

27.8%; Score 128.5;

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Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 IVLALLIVSAALSSVVSRIDSPSPTVLNSHISTPNVRALTHENQTKPSISQISTTLPPTT 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 15.0%; Score 69.5; DB 4; I Similarity 31.9%; Pred. No. 0.8; 21; Conservative 14; Mismatches 22;
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (171)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-481
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CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: DCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
                                                                          EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
                         APPLICATION NUMBER: 60/048,949
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                                                      1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
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US-09-205-258-421
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LENGTH: 171
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                                Gaps
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                                                                                          19 SNSGSNTLENGYFLSRNKENHSOPTOSSLEDSVTPTKAVKTTG 61
      Pred. No. 3.7e-08;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,882
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,892
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,880
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                         Sequence 481, Application US/09205258 Patent No. 6525174
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                                      27; Conservative
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Best Local Similarity
Matches 27; Conserv
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER PELLING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,898
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EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,973
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/09,921
EARLIER FILING DATE: 1997-07-10
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R FILING DATE: 1997-06-06
R PAPLICATION NUMBER: 60/048, 896
R PILLING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049, 020
R PILING DATE: 1997-06-06
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EARLIER FILLIG DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,917

EARLIER FILLING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,949

EARLIER APPLICATION NUMBER: 60/048,949
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APPLICATION WUMBER: 60/048,972
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,916
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,970
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
APPLICATION UNMBER: 60/048,971
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APPLICATION NUMBER: 60/048,900
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICANT: Gong, Joseph K.
APPLICANT: Gong, Joseph K.
APPLICANT: Glonest, Chester A.
APPLICANT: Glonest, Chester A.
TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Aixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
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1. Similarity 27.6%; Pred. No. 6.4;
21; Conservative 15; Mismatches 23; Indels 17
                                                                                                          Length 257;
                                                                                                                                                     22; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: EM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/547,197
FILING DATE:
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REGISTRATION NUMBER: 38,601
REFERENENE/COCKET NUMBER: 19226/580 (R-5228)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
                                                                                                             Query Match
15.0%; Score 69.5; Di
Best Local Similarity 31.8%; Pred. No. 1.4;
Matches 21; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08547197; Patent No. 5691157
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267 VGAQRDAWGPGVAKSS 282
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ATTORNEY/AGENT INFORMATION:
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amino acid
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MOLECULE TYPE: protein
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                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-205-258-421
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Best Local Similarity
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SEQ ID NO 421
LENGTH: 257
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: DEPLDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 0.27946-0.3
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                      Length 354;
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                                                                                                                                                                   14.4%; Score 66.5; DE
25.7%; Pred. No. 5.2;
:ive 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6345, Application US/09134000C
Patent No. 6617156
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                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Enterococcus faecalis
    1998-07-27
                                                                                                                                                                                                                                                                                                                                                                              : | | | | | : | | 130 RGGNLDFEGIACDA 143
                                                                                                                                                                                                                      19; Conservative
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PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 32891
LENGTH: 354
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                           TYPE: PRT
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                        Matches
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ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AEXOGENOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AEXOGENOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 LFKNMEGNCPPSWNIDSSCKLELSQNQNVKLTVNNVLKETRILNIFGVIKGYEBPDRYIV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GIVKGRNLDSRGLI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                    APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
TITLE OF INVENTION: A METHOD FOR DETECTING A RADIOMIMETIC AGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Clinton Square, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68.5; DB 3;
Pred. No. 6.4;
5; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 LSRNKENHSQPT---QSSLEDSVTPTKAVKTTGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32891, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORIEN JAMES ROGALS, PETER NAME: ROGALSKYJ, PETER REGISTATION UNÜBER: 38,601
REFERENCE/DOCKET UNÜBER: 19228
TELECOMMUNICATION INFORMATION: TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                        US-08-957-940-1
; Sequence 1, Application US/08957940
Patent No. 6132981
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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267 VGAQRDAWGPGVAKSS 282
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27.6%;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                   CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND ALINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: BPLDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILLING DATE: 1997-11-08
PRIOR FILLING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

FILE OF INVENTION:

BELGNOON WICKLET CACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION:

FILE REPERENCE:

CURRENT APPLICATION NUMBER:

CURRENT APPLICATION NUMBER:

PRIOR PRING DATE:

1999-01-29

NUMBER OF SEQ ID NOS:

14342

SEQ ID NO 12003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPT--KAVKTTGKGIVKGRN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 WRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKGIVKGRNLDS---R 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 881;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Indels
                                     222 NGKGV---KRLEDIGMIKTVPRTGMEALDTNVSED 253
               83
             -- LGAEAWGRGVKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63.5; DB Pred. No. 44; 7; Mismatches
                                                                                                                                                       ; Sequence 12003, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; sequence 4255, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis US-09-134-001C-4255
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               60 TGKGIVKGRNLDSRGLI---
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Best Local Similarity 29.9%;
Matches 20; Conservative
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286 GAQLASD 292
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                                                                                                                                            US-09-489-039A-12003
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LENGTH: 315
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Best Local S:
Matches 22
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Patent No. 6552294
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering Engrence 17TLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CUBRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1254
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 VVVEDLVVKEHRVTGVVTNWALVSMNQDTHSQ-TQSHMDANVMBAKIVVSSCGHEGLFSA 221
                                          3;
                                                                                                           83 SNVIHPGYGFLSESTNFAKAVEDNHIHFIGPSKTTMEMMGBKITARQTVKQAGVPVIPGS 142
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                                                                                23 SNTLENGY-FLSRN-----KENH-----SQPTQSSLEDSVTPTKAVKTTGKGIVKGR
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                                            Gaps
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                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAV
; Score 65; DB 4; Length 461;
; Pred. No. 12;
10; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAUGULANT: FARGALSKI, O. ADTONI;
APPLICANT: FARGALSKI, J. ADTONI;
TITLE OF INVENTION: Thiamine Biosynthetic Enzymes;
FILE REPERENCE: BB1372 US NA;
CURRENT FILING DATE: 2000-06-15;
PRIOR APPLICATION NUMBER: 60/139,556;
PRIOR PILING DATE: 1999-06-16;
NUMBER OF SEQ ID NOS: 45;
SOFTWARE: Microsoft Office 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TKAVKTTGKGIVKGRNLDSRGLILGAEAWGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 SLLLLLVCEAIWRSNSGSNTLENGYFLSRN---KENHSQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/09594506 Patent No. 6512164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Chlamydia pneumoniae
    Query Match
Best Local Similarity 29.5%;
Matches 18; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Triticum aestivum
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Matches 23; Conserv
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Matches 25; Conserv
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US-09-198-452A-1254
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Search completed: March 31, 2004, 12:16:02 Job time : 24 secs

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March 31, 2004, 12:11:11; Search time 39 Seconds (without alignments) 728:119 Million cell updates/sec
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462
1 MTFFLSLILLLVCEAIWRSN......DSRGLILGAEAWGRGVKKNT 90
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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1: Sp_archea:*
2: sp_bacteria:*
3: sp_fung:*
4: sp_fung:*
5: sp_invertebrate:*
5: sp_invertebrate:*
5: sp_mamal:*
5: sp_mamal:*
5: sp_mhc:*
5: sp_phage:*
5: sp_hage:*
5: sp_hage:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 2000000000
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110:
12:
143:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q96dr9 homo sapien	Q96pa5 homo sapien	Q9bxn2 homo sapien	Q8hzr8 macaca mula	Q9ji50 mus musculu	Q8k1l4 mus musculu	Q8nzp4 streptococc	Q938n5 streptococc	048391 streptococc	Q38585 streptococc	Q8s2u4 medicago sa	Q9sbr7 medicago va	Q8pdr9 xanthomonas	Q928w4 listeria in	Q9vg84 drosophila	Q8mzc0 drosophila
SUMMARIES	ID	Q96DR9	Q96PA5	Q9BXN2	QSHZRB	. Q9JI50	L QBK1L4	5 Q8NZP4	5 Q938N5	048391	Q38585	D Q8S2U4	0 09SBR7	5 QBPDR9	6 Q928W4	Q9VG84	QBMZC0
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e)e	Query Match Length DB	53.6	53.6	53.6	47.1	31.1	29.5	17.3	17.3	16.9	16.7	16.2	15.4	15.2	15.2	15.2	15.2
	Score	247.5	247.5	247.5	217.5	143.5	136.5	80	80	78	77	75	71	70	70	7.0	7.0
	Result No.		7	m	4	ഹ	9	7	83	σn	10	11	12	13	14	15	16

RESULT 2

Qenc54 homo sapien Qenrg2 homo sapien Qe5897 synechocyst Q93291 fugu rubrip Q9kpv7 vibrio chol		09d851 mus musculu 08btr4 mus musculu 057435 fugu rubrip	Q962d2 drosophila Q8intl drosophila	pseudomoma oryza sati oryza sati	influe influe	influenza influenza	Q8az80 influenza a Q919W1 influenza a			·	Q9qnb4 influenzavı
QBNC54 Q9NRG2 Q55897 Q93291 Q9KPV7	O.		$\alpha \alpha$	Q9HUJ9 Q8W3H4 Q7XRV7				09SFE3		2 Q9QNB5 Q8QM08	2 Q9QNB4
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ALIGNMENTS

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"A novel cluster of lectin-like receptor genes expressed in monocytic, dendritic and endothelial cells maps close to the NK receptor genes in the human NK gene complex.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Dendritic cell-associated C-type lectin-1 (DECTIN-1 receptor) (Lectin-
like receptor 1) (Beta-glucan receptor isoform A).
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Yokota K., Takashima A., Bergstresser P.R., Ariizumi K.;
"Identification of a human homologue of the dendritic cell-associated
C-type lectin-1, dectin-1.";
Gene 272:51-60(2001).
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MEDLINE=21381615; PubMed=11491532;
MEDLINE=21381615; PubMed=11491532;
MEDLINE=21381615; PubMed=11491532;
MEDLINE=Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;
"Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene expressed on dendritic cells.";
[munnogenetics 53:288-295(2001).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURNCE FROM N.A. Willment J.A., Gordon S., Brown G.D.; Willment J.A., Gordon S., Brown G.D.; "Characterization of the human beta-glucan receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21130 MW; 6F3350B1DFBEC921 CRC64;
                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta-glucan receptor isoform G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 53.6%; Score 247.5; DB 4; I Similarity 80.6%; Pred. No. 5.9e-19; 50; Conservative 4; Mismatches 3;
                                                  192
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                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alternatively spliced isoforms."
J. Biol. Chem. 0:0-0(2001).
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                                                  PRELIMINARY;
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53 LCLVILVIAVVLGTMAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKT 112
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"Simian Immunodeficiency Virus Dramatically Alters Expression of
Homeostatic Chemokines and Dendritic Cell Markers During Infection In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 LSLLLLLVC----EAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKT
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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                                                                                                               TISSUE-PETIPHERAL Blood leukocytes;
Willment J.A., Gordon S., Brown G.D.;
"Characterization of the human beta-glucan receptor and its alternatively spliced isoforms.";
J. Biol. Chem. 0:0-0(2001).
Herranz-Falcon P., Arce I., Fernandez-Ruiz B.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL; A7312373; CAC43647.1; -...
EMBL; A7312373; CAC43647.1; -...
EMBL; A7312373; CAC43647.1; -...
EMBL; A7026769; AAK20114.2; -...
Genew; HGNC.14558; CLECSF12. ...
GO, GO.0004572; F:receptor activity; IEA.
GO, GO.000157; F:receptor activity; IEA.
GO, GO.000157; F:heterophilic cell adhesion; IAE.
InterPro; IPR002353; AntifreeZeII.
InterPro; IPR00359; Lectin_C.
Fram; PF00059; Lectin_C.
Fram; PF00059; Lectin_C.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Dendritic cell-associated C-type lectin-1.
Macaca mulatta (Rhesus macaque)
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InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_c; 1. PRINTS; PR00356; ANTIFREEZEII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSS0041; C_TYPE_LECTIN_2; 1. Lectin; Receptor. SEQUENCE 247 AA: 27627 Mm. .....
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InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
                                                                                                   29.5%;
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01-OCT-2003 (TEMBLEEL 25,
Hypothetical phage protein 6
SPYMI8 1802.
                                                                                                              59.68;
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                                                                                                   Query Match
Best Local Similarity 59.6
Matches 28; Conservative
                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to C-type (Calcium dependent, carbohydrate recognition domain)
lectin, superfamily member 12.
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20347934; PubMed=10779524; Ms., Ritter R. III, Ariaumi K., Shen G.-L., Shikano S., Xu S., Ritter R. III, Ariaumi K., Shen G.-L., Morita A., Bergstresser P.R., Takashima A.; Rumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.; "Identification of a novel, dendritic cell-associated molecule, dectin-1, by subtractive cDNA cloning."; J. Biol. Chem. 275:20157-20167(2000).

EMBL; AF262995; AAP72710.1; -.
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                                          5 ISILLLLVC-----BAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 244;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO27742; AAH27742.1; -.
GO; GO:0005529; F:sugar binding; IEA.
Pred. No. 1.5e-15; Indels
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                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Dendritic cell-associated C-type lectin-1.
CLECSF12 OR DECTIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1861431; Clecsf12.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
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6; Mismatches 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 143.5;
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61.7%;
          ilarity 71.0%;
Conservative
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Best Local Similarity
Matches 29; Conserv
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            Similarity
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                                                                                                                      113 TG 114
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              Best Local
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MEDLINE=21927593; PubMed=11917108;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Antirepressor (Putative P1-type antirepressor-phage associated).
SPYM3 1261 OR SP80602.
Streptococcus pyogenes and
streptococcus pyogenes (serotype M3).
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                                                                                                                                                             Score 136.5; DB 11; Length 244; Pred. No. 1e-06; 6; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                           68 AFWRHNSGRNPEEKDNFPSRNKENH-KPTESSLDEKVAPSKASQTTG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
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                                                                                                                                                                                                                                                                           15 AIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Hypothetical protein.
SEQUENCE 239 AA; 27449 MW; 91988787A84A9853 CRC64;
Print; Pro0059; lectin c; l. PRINTS; PR00356; ANTIFREEZEII. SMART; SMO034; CLECT. C. TYPE LECTIN 2; l. SPROSTER; PS50041; C. TYPE LECTIN 2; l. SEQUENCE 244 AA; 27542 MW; F50158025FA80C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002)
EMBL, AE010087; AAL98325.1; -. 60; GO:0003677; F.DNA binding; IEA.
InterPro; IPR005039; Anti_rep.
Pfam; PF03374; ANT; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 NSGSNTL----ENGYFLSRNKENHSQPTQSSLE----
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29.7%; Pred. No. 1.5;
tive 11; Mismatches 14;
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EMBL; AF020798; AAC03459.1; -. GO; GO: 0003677; F:DNA binding; IEA.
InterPro: IPRO5039; Anti_rep.
Fram; PF03374; ANT; I.
SEQUENCE 238 AA; 27081 MW; C30F3E97018EE651 CRC64;
                                                                                                                                                                                                                                          20 NSGSNTL-----ENGYFLSRNKENHSQPTQSSLE-
                                                                                                                                               16.9%; Score 78; DB 934.4%; Pred. No. 2.4; iive 6; Mismatches
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EMBL; AF115103; AAD44100.1; --
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR005039; Anti_rep.
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                                                                                                                                                                                          22; Conservative
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01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                    PECIES. Progress. STRAIN-MGAS315 / Serotype M3; MEDIME-22133808; PubMed=12122206; MEDIME-22133808; PubMed=12122206; Medime S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., "Gender P.M., Musser J.M., "Gender Sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98122991; PubMed=9454717;
Neve H., Zenz K.I., Desiere F., Koch A., Heller K.J., Brussow H.;
"Comparison of the lysogeny modules from the temperate streptococcus
thermophilus bacteriophages TP-034 and sfi21: implications for the
modular theory of phage evolution.";
Virology 241:61-72(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S. Programs; STRAIN=SSI-1 / Serotype M3;

Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,

A Hayashi H., Hamada S.;

"The genome of invasive Streptococcus pyogenes; a comparative analy
of S. Pyogenes SSI-1, SF370 and MGASB222.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BEML; ARO50245; AALI5047.1; -.

BEML; ARO50245; AALI5047.1; -.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R PFam; PF03374; ANT; 1.

RR PFam; PF03374; ANT; 1.

RR PFam; PF03374; ANT; 1.

RR PFam; PF03774; SNA; 27843 MW; SAAB5551447E366C CRC64;
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Streptococcus thermophilus bacteriophage TP-J34.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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                                                                                                           SPECIESS. Progenes, STRAIN-NIHI;
Ikebe T., Wada A., Inagaki Y., Sugama K., Tanaka D., Suzuki
Katsukawa C., Fujinaga Y., Abe Y., Watanabe H.;
"Complete sequence of temperate phage PhinIHI.1.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 242;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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Pred. No. 1.5;
5; Mismatches
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35.9%;
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                                             NCBI_TaxID=1314, 198466;
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                                                                                          SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDIINE=98160788; PubMed=9499809;
Desiere F., Lucchini S., Brussow H.;
"Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Desiere F., Lucchini S., Bruttin A., Brussow H.;
"Streptococcus thermophilus bacteriophage Sfi21 complete genome.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus thermophilus bacteriophage Sfi21.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VGBI_TaxID=64186;
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MEDLINE=96204576; PubMed=8623559;
MEDLINE=96204576; PubMed=8623559;
Brutin A., Bruessow H.;
"Site-specific spontaneous deletions in three genome regions of temperate Streptococcus thermophilus phage.";
Virology 219:96-104(1996).
                                                                 20;
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DB 9; Length 238;
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                                                          16; Indels
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SEQUENCE 287 AA; 33148 MW; 49651DA8F986CF50 CRC64;
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Last annotation update)
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RECOMMENDATE STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN
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STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21237279; PubMed=11679669;
MEDLINE=21237279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
                                                                                                                                                                                                     Xanthomonas campestris (pv. campestris).Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;Xanthomonadaceae; Xanthomonas.
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NCBL_TaxID=1642;
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                                                                                                          Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein lin2418.
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15;
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GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR000379; Ser_estrs.
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Pred. No.
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                                                                                   Created)
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27.2%;
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                                   PRELIMINARY;
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Nature 417:459-463(2002)
                                                                                 (TrEMBLrel,
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            NCBI_TaxID=340;
                                                                            01-OCT-2002 (01-OCT-2002 (01-OCT-2003 (
                                                                                                                                                                                                   Xanthomonas
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            Q8PDR9
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MEDLINE=20120383; PubMed=10656590;
MEDLINE=20120383; PubMed=10656590;
"Expression profiles of 22 novel molecular markers for organogenetic pathways acting in alfalfa nodule development.";
Mol. Plant Microbe Interact. 13:96-106(2000).
                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
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Medicago varia,
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                                                                                                             [1] -
SEQUENCE FROM N.A.
Kevel Z., Vinardell J.M., Kiss G.B., Kondorosi A., Kondorosi E.;
Kevel Z., Vinardell J.M., Kiss G.B., Kondorosi E.;
"Glycine-rich proteins encoded by a nodule-specific gene family are
implicated in different stages of symbiotic nodule development in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 AA; 23496 MW; 9B39BE481624C19D CRC64;
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NCE 213 AA; 23149 MW; 137C629ED1D9872A CRC64;
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                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Nodule-specific glycine-rich protein 3.
Medicago sativa (Alfalfa).
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  PRT;
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13,
22,
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Conservative
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Best Local Similarity 30.19
Matches 31; Conservative
PRELIMINARY;
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01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 32; Conserv
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ENODGRP5.
                                                                                                                                                                                                                                         NCBI_TaxID=3879;
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RESULT 12

à g à g Q9SBR7

----KENHSQPTQSSLED-

24;

Length 205; 30; Indels

16;

RESULT 13

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REDINE = BY CREALLY;

RA Addams N.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addams N.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addams N.D., Celliker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Addams O.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Button G.G., Rocrers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Barman B.D., Blankov S.,

RA Barlew R.M., Bounck J., Bornan B.D., Blotherson S.N.,

Borkova D., Botchan M.R., Bounck J., Brokstein P., Brottier P.,

RA Burris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,

RA Chorin B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,

Burbin K.J., Evangelista C.C., Ferrierz S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Rarpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Liu X., Mattei B.E., McIntcosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Mazny D.M., Nelson D.L.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Nos E., Nodjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
"Comparative genomics of Listeria species.";
Comparative genomics of Listeria species.";
Science 294:849-882 (2001).
PIR: ABJ734, ABJ734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSYG84,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CGI7227 protein (EC 6.5.1.1) (DNA ligase) (Polydeoxyribonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||| :|| :|| ::::||| |:| :
190 QNGYLISRRGTDYNRPTQKSMELGLFKIKETAIMRSSGAHTAITAKVTGKG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 ENGYFLSRNKENHSQPTQSSLEDSVTPTK-------AVKTTGKG 63
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03374; ANT; 1. Pfam; PF02499; Bro-N; 1. Hypothetical protein; Complete protecme. SEQUENCE 256 AA; 29082 MW; SFE3FBCFEC81A8B6 CRC64;
                                                                                                                                                                                                                                                 Listilist, LINO2418, --
GO, GO:0003677, F:DNA binding, IEA.
InterPro, IPR005039, Anti_rep.
InterPro, IPR003497; BRO_Nterm.
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Matches 16; Conservative
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NCBI_TaxID=7227;
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Barans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Barans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Reriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Riphiams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shenington K., Saunders R.D.C., Scheeler F., Shen H., She B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woorley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zhong K.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TherePro; IPRO00977; DNA_ligase.

Fram; PF01069; DNA_ligase. 1.

Fram; PF04675; DNA_ligase. A.C.; 1.

Pfam; PF04675; DNA_ligase. A.C.; 1.

Pfam; PF04675; DNA_ligase. A.N.; 1.

TIGRFAMS; TIGR00574; dnl1; 1.

PROSITE; PS00133; DNA_LIGASE A.N.; 1.

PROSITE; PS00133; DNA_LIGASE A.N.; 1.

PROSITE; PS00104; DNA_LIGASE A.N.; 1.

PROSITE; PS00104; DNA_LIGASE A.N.; 1.

AIP-binding; DNA_recombination; DNA_repair; DNA_replication; Ligase.

SEQUENCE 661 AA; 73899 WW; SC5711C0AF2D7F27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hardecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Shith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter C.J.;
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EMBL; AB005695; AAF54001.2; -.

Flybase; Fegnot038035; CG17227.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005910; F:DNA ligase (ATP) activity; IEA.

GO; GO:0005814; F:ligase activity; IEA.

GO; GO:0005819; P:DNA recombination; IEA.

GO; GO:000581; P:DNA repair; IEA.

GO; GO:0005260; P:DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIYBASE;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE) (N) +
{DEOXYRIBONUCLEOTIDE} (M) = AMP + DIPHOSPHATE +
{DEOXYRIBONUCLEOTIDE} (N+M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Vente
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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15.2%; Score 70; DB 5; Length 661;

Query Match

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2,
                       8; Gaps
Best Local Similarity 31.7%; Pred. No. 63;
Matches 20; Conservative 12; Mismatches 23; Indels
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73		596
NLDSR		PKEDE
GIVKGR		- WKKE
VKTTGK		FKS
VTPTKA		FKPSKE
STEDS	••	SLKDF
-OPTOSS		PSOKC
0		AIRSLSPS
ENHS		ESK
SRNK		SKRKESK
NGYFL		APVI
ATLE		ODED
RSNSGSI	- - -	RSNTGSDDEDG
18		541

⁷⁴ GLI 76 δλ

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Search completed: March 31, 2004, 12:14:55 Job time : 41 secs

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March 31, 2004, 12:07:20 ; Search time 54 Seconds (without alignments) 470.913 Million cell updates/sec
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462
1 MTFFLSLLLLLVCEAIWRSN......DSRGLILGAEAWGRGVKKNT 90
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		1 6 6	PRO	PRO	PRO	PRO	PRO	hum	Sec	hum	sec	PRO	PRO	hum	PRO	sec	Sec	PRO	sec	sec	hum	hum	sec	hum	PRO	hum
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	Description	Aav66748	46	Aau12408	Aab50922	Aab65271	Abu58086	Abu59164	Abu82676	Abo17852	Abu60595	Abu13977	Abu81106	Abu72562	Abu66806	Abu59887	Abu59311	Abo26008	Abo25077	Abu59017	Abu92395	Abu59460	Abu67082	Abu92226	Abu10932	Abu81684
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SUMM	Ω	AAY6674	9	AAU1240	AAB5092	AAB6527	ABU5808	ABU5916	ABU8267	AB01785	ABU6059	ABU1397	ABU81106	ABU72562	ABU66806	ABUS9887	ABU5931	ABO26008	AB02507	ABU5901	ABU92395	ABU59460	ABU67082	ABU92226	ABU1093	ABU8168
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6 6 6 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1.1 (V667.10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8;	05-APR-2000 (first en	-bound prote	Membrane-bound polypept. pharmaceutical; recepto: Homo sapiens.	WO9963088-A2.	09-DEC-1999.	02-JUN-1999; 99WO-US	1998; 98 1998; 98 1998; 98	-JUN-1998; 98US-0		-JUN-1998; 98US-0 -JUN-1998; 98US-0	-JUN-1998; 98US-0	-JUN-1998; 98US-0 -JUN-1998; 98US-0	-CON-1998; 98US-0 -JUN-1998; 98US-0 -JUN-1998: 98US-0	-JUN-1998; 98US-0	-JUN-1998; 98US-0	- 2005 (8605-000-0000-0000-0000-0000-0000-0000-0		-JUN-1998; 98US-0
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98US-0096143P.
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             11-AUG-1998;
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26-AUG-1998
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### (GETH ) GENENTECH INC.

Watanabe CK; Smith V, Gurney AL, Goddard A, Chen J, Yuan J; Baker K, Wood WI,

WPI; 2000-072883/06. N-PSDB; AAZ65094.

Membrane-bound proteins and related nucleotide sequences

Claim 12; Fig 272; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polymucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadheeins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

#### Sequence 90 AA;

Gaps . 0 Length 90; 0; Indels 100.0%; Score 462; DB 3; 100.0%; Pred. No. 9.8e-49; iive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 90; Conservative

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Homo sapiens
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                                                                                                                    Human PRO1159 protein UNQ589 SEQ ID NO:273
                                                                                                                                                                                                                                                    graft rejection; graft-versus-host-disease
      GKGIVKGRNLDSRGLILGAEAWGRGVKKNT
                   GKGIVKGRNLDSRGLILGAEAWGRGVKKNT
                                                                AAB33469 standard; protein; 90 AA
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                                                                                                                                                                                                                                                                                    WO200053758-A2.
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                     02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1999;
28-JUL-1999;
01-SEP-1999;
                                                                                                  29-JAN-2001
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15-SEP-1999;
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                                                                                                                                                                                                                                                                                                     14-SEP-2000
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                     61
                                                                                  AAB33469;
      61
                                              RESULT 2
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lummune related disorders. The disorders are selected from systemic lummune related disorders, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Siogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated sensil disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune correlated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACS8397 to AACS858 cyrepresent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS879 to AACS8642 and AAB33477 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                            Gurney AL, Hebert C, Henzel W;
D, Shelton DL, Smith V;
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIFFLSLLLLLUCEALWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTFTKAVKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 462; DB 3;
100.0%; Pred. No. 9.8e-49;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 90
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                                                                                                                                                                                                                                               Goddard A,
J, Pennica
                                                                                                                                                                                                                                                                                                                Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO1159 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 33; Fig 112; 309pp; English.
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
                                                                                                    22-FEB-2000; 2000WO-US004414
                                                                                                                                                                                                                                            Baker KP, Go
Ju Y, Pan J,
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                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                            Stewart TA, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-572271/53.
                                                                                                                                                                                                                                                                               Lu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC58634.
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                                                                                                                                                                                                                                        Ashkenazi AJ,
Kabakoff RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU12408;
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Claim 12; Fig 474; 813pp; English.
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2000US-0187202P.
2000WO-US006319.
2000WO-US006884.
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2000WO-US013705.
2000WO-US014042.
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2000MO-US014042.
2000MO-US014941.
                                                               99WO-US028564
99WO-US028565
                                                                              99US-0170262P
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2000WO-US004414
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2000WO-US007532
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2000US-0209832P
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                                                                                                                                                                                                                                                                                                                                                                                                                             breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                      GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                    Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                  2001-408281/43.
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WO200140466-A2
                                                                                                                                             11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME,
                                                                                    16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
30-DEC-1999;
                                                                                                                        05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
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03-MAR-2000;
10-MAR-2000;
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05-JUN-2000;
28-JUL-2000;
                            01-DEC-2000;
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01-MAR-2000;
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21-MAR-2000;
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                                                                               09-DEC-1999
              07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                     Baker KP,
                                                                                                                                                                                                                                                                                                                                                                    Smith V,
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proliferation of inner ear utricular supporting cells or of T-
lymphocytes, the release of a cytokine from peripheral blood monocytes
(PBMCs), or the proliferation of endothelial cells. Some of the PRO
polypeptides may modulate glucose or free fatty acid uptake by skeletal
muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
VITA. The PRO polypeptides can be used in assays to identify molecules
involved in binding interactions. The polynucleotides encoding PRO
polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTFFLSLLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTFFLSLLLLTVCBAIMRSNSGSNTLENGYFLSRNKENHOOPTQSSLEDSVTPTKAVKTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidiabetic; noctropic; neuroprefective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO; antiinflammatory; dermatological; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 462; DB 4; Length 90; 100.0%; Pred. No. 9.8e-49; ive 0; Mismatches 0; Indels
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99US-0144758P.
99US-0146222P.
99WO-US020111.
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2000WO-US003565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 100.
90; Conservative
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                                                                                                                                                                                                                                                                                                                                         Sequence 90 AA;
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18-FEB-2000;
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29-OCT-1999;
30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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XXX AAB5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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4E, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000WO-US005601 2000WO-US005841

01-MAR-2000; 02-MAR-2000;

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2000US-0187202P

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The present equations is one of this of the inver invo purpoputures. The present equations is one of the present equations and diagnosing immune related disorders such as useful for treating and diagnosing immune related disorders such as experimentations, rheumatorid archiritis, orthorid archiritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic sclerosis, ascoidosis, autocimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple solerosis, didopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis, confection and urticaria, immunological diseases such as sethma, allergic rhinitis, acopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung controding graft rejection and graft-versus-host diseases
                                                                                                                                                                                                                                                                                                                 Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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Shelton DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO1159 (UNQ589) protein sequence SEQ 1D NO:377.
                                                                                                                                                                                       Goddard A,
Kabakoff RC,
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                                                                                                                                                                                   f, Baker KP, Chan B,
Hebert C, Henzel W,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 58; Fig 42; 218pp; English.
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2000WO-US008439.
2000WO-US013705.
                 2000WO-US006884
2000WO-US007377
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N-PSDB; AAC91481.
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Best Local Similarity
Matches 90; Conserv
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Watanabe CK,
                                                   21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
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               15-MAR-2000;
20-MAR-2000;
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO mucleotide cadiolabels or antibodies, that cause cell death. PRO mucleotide cadiolabels or antibodies, in the generation of anti-sense RNA and chromosomal and gene mapping, and in the generation of anti-sense RNA and chromosomal and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Auti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44401 represent PCR primares and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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Paoni NF;
Wood WI;
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 chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Fig 272; 935pp; English.
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2000WO-US000219.
2000WO-US000376.
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99US-0141037P
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99US-0145698P
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99US-0149396P
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Tra N, Fong S,
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              diagnostic assay.
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Grimaldi CJ,
Roy MA, Stewa
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
                                           Homo sapiens.
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02-MAR-2000;
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Gaps

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Indels

Length 90;

100.0%; Score 462; DB 4; 100.0%; Pred. No. 9.8e-49; live 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 90; Conservative

us-09-989-293a-377.rag

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98US-0089538P

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25-JUN-1998;
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12-AUG-1998;
17-AUG-1998;
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17-AUG-1998;
17-AUG-1998;
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              MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT
                                    1 MIFFLSLLLLUCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVIPTKAVKIT
                                                                                                                                                                                                                                                                             Human, PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
                                                                  GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 90
                                                                                  GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 90
                                                                                                                                                                  ABUS8086 standard; protein; 90 AA
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970S-0062250P.
970S-0065186P.
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980S-0083322P.
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                                                                                                                                                                                                                                                    Human PRO polypeptide #118
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15-NOV-1997)
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1 MIFFLSLLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60
                                                                                                                                                                            Human; PRC; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; cfos induction; vascular endothelial growth factor inhibition; VEGF inhibition; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                                                                                                                                                         Novel human secreted or transmembrane protein PRO1159.
                                          90
                     61 GKGIVKGRNLDSRGLILGABAWGRGVKKNT 90
                                   61 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT
                                                                                            ABUS9164 standard; protein; 90 AA.
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97WS-00531BP.
97US-006531BP.
97US-0065312P.
98US-0075945P.
98US-0075945P.
98US-008332P.
98US-0087106P.
98US-0087600P.
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98US-0088021P.
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98US-0088326P.
98US-0088167P.
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98US-0088212P.
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98US-0088655P.
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98US-0088742P.
98US-0088810P.
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98US-0088028P.
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98US-0088826P
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24-NOV-1997;
25-FEB-1998;
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28-MAY-1998;
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100.0%; Score 462; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0;
                                      98US-0097022P.
98US-0097141P.
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99US-0149396P.
99WO-US021090.
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98US-0100858P.
98WO-US019437.
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98US-0088858P. 98US-0088861P. 98US-0088876P.

11-JUN-1998;

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Gaps

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Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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          9805-0089512P-9805-0089512P-9805-0089512P-9805-0089532P-9805-0089598P-9805-0089653P-9805-0089653P-9805-0089653P-9805-0089653P-9805-0089653P-9805-0089653P-9805-0089603P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899903P-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9805-00899907-9
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15-MAR-2000;
20-MAR-2000;
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15-MAY-2000;
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22-MAY-2000;
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28-JUL-2000;
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24-FEB-2000;
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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in complete a security molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. Solution of the contains a cardiac insufficiency discorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO136, PRO943, PRO943, PRO926, PRO1068 or PRO535, PRO943, PRO928, PRO926, PRO1068 or PRO535, PRO943, PRO9387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are comported in growth factor (VEGF) stimulated proliferation of endothelial growth factor (VEGF) stimulated proliferation of endothelial colls and is thus useful for inhibiting endothelial cells growth in mammals which would be beneficial in inhibiting tumour growth. PRO926, PRO1184, PRO1364 and Are therespentically useful for enhancing communication of estimulated T-lymphocytes and are these proliferation of stimulated T-lymphocytes and are these proliferation of stimulated T-lymphocytes and are these proposes in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propose in the propo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retinal neurons cells (PRO1132 is also enhances survival/proliferation of red photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinits pigenetosum, AMD. PRO819, PRO813 and PRO810 feration of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cells, such therefore as associated with dermaritis, herpetiformis or crohn's disease. PRO1310, PRO812, PRO1192 and PRO1387 induce the proliferation and/or reddifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein
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100.0%; Pred. No. 9.8e-49;
iive 0; Mismatches 0;
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Claim 12; Fig 272; 648pp; English
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DL; Godowski PJ; Paoni NF; Wood WI;

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98US-0090863P. 98US-0091360P. 98US-0091360P. 98US-0091513P. 98US-0091513P. 98US-0091513P. 98US-0091533P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-009614FP. 98US-0
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15-MAR-2000; 2000WO-US006894.
20-MAR-2000; 2000WO-US006843.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013386.
17-MAY-2000; 2000WO-US013398.
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02-JUN-2000; 2000WO-US015264.
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                                    08-0CT-1999;
30-NOV-1999;
01-DEC-1999;
16-DEC-1999;
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06-JAN-2000;
11-FEB-2000;
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1 MTFFLSLLLLVCEAIWRSNSGSNTLENGYPLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency syndrome (AIDS), or cancer.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                 09-MAR-2001; 2001US-00802706; 22-MAR-2001; 2001US-00802706; 22-MAR-2001; 2001US-00802706; 22-MAY-2001; 2001US-00854208; 10-MAY-2001; 2001US-00854208; 10-MAY-2001; 2001US-00854209; 18-MAY-2001; 2001US-00866028; 25-MAY-2001; 2001US-00866028; 25-MAY-2001; 2001US-00866028; 25-MAY-2001; 2001US-00866034; 25-MAY-2001; 2001US-00866034; 25-MAY-2001; 2001US-0086634; 19-JUN-2001; 2001US-00896342; 20-JUN-2001; 2001US-00886342; 20-JUN-2001; 2001US-00886342; 22-JUN-2001; 2001US-008863636; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-0088779; 22-JUN-2001; 2001US-008877879; 22-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-008877879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001US-00887879; 23-JUN-2001; 2001U
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ME, Goddard A,
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Best Local Similarity 100.0
Matches 90; Conservative
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N-PSDB; ACD24089.
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09-JUL-2001;
18-JUL-2001;
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Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
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90
                               61 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT
61 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT
                                                                                                                                                                                                                                                                                                                             diagnostic; therapeutic; gene therapy.
                                                                                                                                          ABU60595 standard; protein; 90 AA
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98US-0084600P.
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12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
25-FEB-1998;
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28-APR-1998;
07-MAY-1998;
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100.0%; Score 462; DB 6; Length 90; 100.0%; Pred. No. 9.8e-49;

0; Gaps

Indels

· 0

0; Mismatches

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The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
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Ferrara N, Fong S, Gerber H, Gerriteen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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2000WO-US004914.
2000WO-US005004.
2000WO-US005841.
2000WO-US006319.
98US-0089599P.
98US-008960P.
98US-008961P.
98US-0089907P.
98US-0089908P.
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2001US-00941992
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99WO-US030095
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2000WO-US000219.
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99WO-US028313
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20-MAR-2000;
30-MAR-2000;
15-MAY-2000;
17-MAY-2000;
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02-JUN-2000;
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111-AUG-2000;
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16-DEC-1999;
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polynucleotides are also useful in gene therapy, in chromosome deditication, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ABU60478-ABU60624 are the PRO polymucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PRO polypeptide, secreted protein; transmembrane protein; genetic disorder; antibacterial; immunosuppressive.
                                                                                                                                                                                                           0;
                                                                                                                                                                                 100.0%; Score 462; DB 6; Length 90; 100.0%; Pred. No. 9.8e-49;
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970S-0065311P
970S-0066770P
980S-0078910P
980S-0083322P
980S-008342P
980S-0083600P
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98US-0088326P.
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97WO-US020069.
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Best Local Similarity
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05-JUN-1998;
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05-NOV-1997;
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25-FBB-1998;
26-FBB-1998;
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07-MAX-1998;
28-APR-1999;
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DL; Godowski P Paoni NF; Wood WI;

Eaton

N. Y. Paoni Wood

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The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
colypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
polypeptides are useful sexpressing PRO polypeptides, for linking
compared to calls expressing PRO polypeptides, for modulating
compared agonists or antagonists. The polymucleotide sequences
conciding PRO polypeptides are useful as hybridisation probes, in
chromosome and gene mapping, in the generation of antisense RNA and DNA,
control of PRO polypeptides, for generating transgenic animals
control of PRO polypeptides, for generating transgenic animals
control of PRO polypeptides, and for the genetic analysis of
cindividuals with genetic disorders, in one therapy, for chromosome
cidentification, as chromosome markers, and for generating probes for PRO
control of PRO polypeptides and Western analysis, ABU13660-
ABU14006 represent the human PRO polypeptides of the invention. Note: The
csequence data for this patent was obtained in electronic format directly
control of the USPTO web site at sequata.uspto.gov/psipsDIDEntry.html
                                                                                      Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-PRO antibody; diagnostic assay, gene expression, diabetes, bone disorder, cartilage disorder, rheumatoid arthritis, obesity; sports injury, osteoarthritis, hyper-insulinaemia; hypo-insulinaemia; hypo-insulinaemia; harr attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO polypeptide; secreted and transmembrane protein;
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 MA, Pan
Williams
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 Kljavin IJ, Napier
mas D, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 90
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                                                                                                                                             Claim 12; Fig 272; 649pp; English.
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             Tumas
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  Ā,
             Stewart TA,
                                                    WPI; 2003-102117/09.
                                                                  N-PSDB; ABX64187
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 Grimaldi
               Roy MA,
Zhang Z;
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Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
98US-0088217P.
98US-0088217P.
98US-0088734P.
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2001US-00941992
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17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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24-FEB-2000;
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20-DEC-1999;
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99WO-US020944
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01-DEC-1998;
05-JAN-1999;
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24-0CT-1997;
24-0CT-1997;
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-SEP-1999;
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12-JUN-1998;
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24-SEP-1997;
17-OCT-1997;
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The present invention relates to the isolation of novel human PRO polypeptides and the polymclectide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polymclectides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis) obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUSB0870-ABUSB1144 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequata.uspto.gov/psipsDIDEDILTy.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTFFLSLLILLVCBAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTFFLSLLLLLVCEAIMRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT
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100.0%; Pred. No. 9.8e-49;
iive 0; Mismatches 0;
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                              99WO-US023089.
99WO-US028214.
99WO-US028313.
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99WO-US028301.
99WO-US028634.
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99WO-US028565.
99WO-US030095.
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
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24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
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99WO-US031243,
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Best Local Similarity luv..
Best a 90, Conservative
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N-PSDB; ACA67230.
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Gerritsen ME,
Smith V, Stewa
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16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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29-NOV-1999;
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or

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virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy; cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease; drug screening.
                                                                      Novel human secreted and transmembrane protein PRO1159
                 ABU72562 standard; protein; 90 AA
                                                                                                                                                                                                                                                           9703-0065311P

9703-0065311P

9803-0083322P

9803-0084600P

9803-0087607P

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9803-008762P

9803-008023P

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97US-0062250P.
97WO-US020069.
97US-0065186P.
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                                                    (first entry)
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17-JUN-1998;
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28-MAY-1998;
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20-MAR-1998;
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                                   ABU72562;
RESULT 13
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2000WO-US005841.
2000WO-US006319.
2000WO-US006884.
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; 2001WO-US019692.
; 2001WO-US021066.
; 2001WO-US021735.
; 2001US-00941992.
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2000WO-US030952.
2000WO-US032678.
2001WO-US006520.
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2000WO-US004414.
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2000WO-US013358.
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29-JUN-2001;
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02-MAR-2000;
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28-FEB-2001;
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11-FEB-2000;
                        07-CCT-1998;
01-DEC-1998;
05-JAN-1999;
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02-JUN-1999;
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15-SEP-1999;
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16-DEC-1999;
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02-JUN-2000;
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            16-SEP-1998;
17-SEP-1998;
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### (GETH ) GENENTECH INC.

DL; Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Perratra M, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi UC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Roy MA, Zhang Z;

### WPI; 2003-352829/33. N-PSDB; ACA64409.

New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's disease

## Claim 12; Fig 272; 663pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colocected cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's

8X333333333X8

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28-FEB-2001; 2001W3-00795498.
28-FEB-2001; 2001W3-00796498.
01-MAR-2001; 2001W3-0080520.
09-MAR-2001; 2001W3-00802706.
22-MAR-2001; 2001W3-00808689.
22-MAR-2001; 2001W3-0081846.
05-APR-2001; 2001W3-00818366.
10-MAY-2001; 2001W3-00854280.
119-MAY-2001; 2001W3-00854280.
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99WO-US031243.
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16-DEC-1999;
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         particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human CDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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disease in mammals. The PRO polypeptides are useful in drug screening,
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
                                                                                                                                  100.0%; Score 462; DB 6; Length 90; 100.0%; Pred. No. 9.8e-49; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                           GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 90
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99WO-US021090.
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                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                              Sequence 90 AA;
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14-JUL-1998;
28-AUG-1998;
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-APR-1999;
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US2003017563-A1

Gao W;

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to calls expressing PRO polypeptides, for modulating bioactive molecules to calls expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation of antisense RNA and genetic disorders, and in gene therapy. ABU665804 represent the human PRO polypeptides of the invention. Note: The sequence data for this parents may a manner of the invention. Here is a genence data for this are sendars mather or who way the unstrument.
                                                                                                                                                                                                                                                                    therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
                                                              Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                             New secreted and transmembrane PRO nucleic acids, useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 474; 660pp; English.
                                                                                                Goddard
                                                                      Beresini M,
                                                                                             Gerritsen ME, Goddaró
Smith V, Stewart TA,
                       (GETH ) GENENTECH INC.
                                                                                                                                                                    WPI; 2003-332040/31.
N-PSDB; ACA03839.
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                                                                      Baker KP,
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1 MTPPLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60 1 MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60 0; Gaps 100.0%; Score 462; DB 6; Length 90; 100.0%; Pred. No. 9.8e-49; Indels ó 0; Mismatches 61 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 90 GKGIVKGRNLDSRGLILGAEAWGRGVKKNT 100.08; 90; Conservative Best Local Similarity Query Match Matches ð a ð g

Novel secreted and transmembrane protein PRO1159. ABUS9887 standard; protein; 90 AA 13-MAY-2003 (first entry) ABU59887; RESULT 15 ABU59887

Human; PRO; hypertrophy of neonatal heart, angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigenentoeum; kidney disorder; meammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.

Homo sapiens

98WO-US012456. 98WO-US014552. 98WO-US017888. 2000WO-US008439 24-AUG-2000; 2000WO-US023328 08-NOV-2000; 2000WO-US030952 2000WO-US003565 2000WO-US004341 2000WO-US006319 2000WO-US006884 2000WO-US014042 98WO-US019093. 98WO-US019330. 98WO-US019437. 99WO-US028565 99WO-US030911 99WO-US030999 99WO-US030720 2000WO-US000376 2000WO-US004414 2002US-00140808 98WO-US018824 98WO-US019177 98WO-US021141 98WO-US022991 98WO-US022992 98WO-US024855 98WO-US025108 99WO-US000106 99WO-US005028 99WO-US008615 99WO-US010733 99WO-US012252 99WO-US020111 99WO-US020594 99WO-US020944 99WO-US023089 99WO-US028214 99WO-US028313 99WO-US028409 99WO-US028301 99WO-US028634 99WO-US028564 99WO-US031274 2000WO-US004342 2000WO-US005601 2000WO-US005746 18-FEB-2000; 22-FEB-2000; 20-MAR-2000; 16-DEC-1999; 20-DEC-1999; 20-DEC-1999; 11-FEB-2000; 24-FEB-2000; 10-SEP-1998; 14-SEP-1998; 14-SEP-1998; 14-SEP-1998; 16-SEP-1998; 17-SEP-1998; 29-NOV-1999; 30-NOV-1999; 30-NOV-1999; 06-JAN-2000; 07-MAY-2002; 05-JAN-2000; 22-DEC-1999; 30-DEC-1999; 30-DEC-1999; 08-SEP-1999 15-SEP-1999 15-SEP-1999 01-DEC-1999 23-JAN-2003 28-AUG-1998 07-OCT-1998 29-OCT-1998 29-OCT-1998 20-NOV-1998 08-MAR-1999 02-JUN-1999 01-SEP-1999 05-0CT-1999 01-DEC-1999 02-DEC-1999 

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10-NOV-2000/, 2000WG-US030873.
10-NOV-2000/, 2000WG-US030873.
20-DEC-2000/, 2000WG-US03456.
28-FEB-2001/, 2001WG-US034556.
28-FEB-2001/, 2001WG-US005520.
10-MAR-2001/, 2001WG-US005666.
10-MAR-2001/, 2001WG-US005666.
10-MAR-2001/, 2001WG-00816744.
10-MAY-2001/, 2001WG-00816744.
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10-MAY-2001/, 2001WG-00816744.
10-MAY-2001/, 2001WG-00816748.
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11-MAY-2001/, 2001WG-0081678.
11-MAY-2001/, 2001WG-0081678.
11-MAY-2001/, 2001WG-0081678.
11-MAY-2001/, 2001WG-008166034.
11-MAY-2001/, 2001WG-008166034.
11-MAY-2001/, 2001WG-0081678.
11-MAY-2001/, 2001WG-008178.
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11-MAY-2001/, 2001WG-008178.
11-MAG-2001/, 2001WG-008178.
11-MAG-2001/, 2001WG-009178.
11-MAG-2001/, 2001WG-009178.
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### (GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-148238/14. N-PSDB; ABX89377.

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

# Claim 12; Fig 474; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO134 and PRO136, PRO943, PRO926, PRO926, PRO168 or PRO535, PRO926, PRO9196, PRO9196, PRO926, PRO168 or PRO535, PRO926, PRO9196, PRO9196, PRO9196, PRO186 and PRO187, Induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO912 inhibits vascular useful for the useful for inhibiting endothelial cell growth in protone for inhibiting tumour growth. PRO826, PRO1966, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, PRO196, Inhibiting pigmentosum, AMD. PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PRO819, PR

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disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein
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                                                                                                                                                                                                                                                1 MTFFLSLLLLVCBAIMRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60
                                                                                                                                                                                                                           1 MTFFLSLLLLLVCEALWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     .0
                                                                                                                                           100.0%; Score 462; DB 6; Length 90; 100.0%; Pred. No. 9.8e-49; ive 0; Mismatches 0; Indels
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APPLICANT: Paul, Nicholas F.
APPLICANT: Stewart, Timchy A.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Anny Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/989,722 CURRENT FILING DATE: 2001-11-19
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Patent No. US20020072067A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1997-10-17
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Gurney, Austin L.
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Eaton, Dan L.
Ferrara, Napoleone
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Paoni, Nicholas F.
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Goddard, Audrey
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Botstein, David
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  Fong, Sherman
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273,0P1GS:
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
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Eaton, Dan L.
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PRIOR APPLIANCY UNDERS.

PRIOR APPLICATION NUMBER: 60/090254

PRIOR FILING DATE: 1998-06-22

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APPLICATION NUMBER: 60/090252
APPLICATION NUMBER: 60/089532
                            ING DATE: 1998-06-17
SICATION NUMBER: 60/089538
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062260
PRIOR PELING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
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Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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Botstein, David
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GENERAL INCORMATION:
APPLICANT: Ashkenazi, Avi J.
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CURRENT FILING DATE: 2001-11-20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 377, Application US/09989731; Patent No. US20020103125A1; GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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Paoni, Nicholas F.
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 1097-06.16
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PRIOR PILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-11-12
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Matches 90; Conservative 0; Mismatches
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
        PRIOR APPLICATION NUMBER: 60/091978
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1996-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi J.
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Botstein, David
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Eaton, Dan L.
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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PRIOR PILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
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Patent No. US20020132252A1
GENERAL INFORMATION:
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Watanabe, Colin K.
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                                    Query Match
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Botstein, David
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Eaton, Dan L.
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Length 90;

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Query Match Best Local Similarity

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC17
1 MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT
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CURRENT FILING DATE: 2001-11-14
PRIOR PEDELICATION NUMBER: 05/049767
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
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Grimaldi, J. Christopher
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APPLICANI: Zhang, Zemin 1.

APPLICANI: Zhang, Zemin 1.

TITLE OF INVENTION: Scoreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PILOR FOR THE REPRENCE: P2730PLC25
CURRENT APPLICATION NUMBER: 05/04993,604
CURRENT APLICATION NUMBER: 60/049787
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Patent No. US20020137075A1
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Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Ferrara, Napoleone
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Tumas, Daniel
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APPLICANT: TARANG, SECRETEd and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: US/09/990,456

CURRENT FILING DATE: 2001-11-14

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i Sequence 377, Application US/09990456
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; APPLICANT: Abhrenazi, Avi J.
: APPLICANT: Baker Kevin P.
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Gurney, Austin L.
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Paoni, Nicholas F.
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Tumas, Daniel
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Wood, William I.
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Eaton, Dan L.
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R APPLICATION NUMBER: 60/090349

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R APPLICATION NUMBER: 60/090357

R APPLICATION NUMBER: 60/090358

R APPLICATION NUMBER: 60/090429

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HITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
HITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
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R APPLICATION NUMBER: 60/087827
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
                                            Sequence 377, Application US/09989721 Patent No. US20020142961A1
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FILING DATE: 1998-06-04
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
Ferrara, Napoleone
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                                                                                   GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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            APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088742
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-13
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PRIOR PRILING DATE: 1998-06-04
PRIOR PRILING DATE: 1998-06-04
Sequence 377, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Botstein, David
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Eaton, Dan L.
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APPLICATION NUMBER: 60/092182
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089599
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08858
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088655
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                    APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/090863
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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478 R APPLICATION NUMBER: 60/090676
R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-24
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R PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/092182 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 1998-07-07 FILING DATE: 1998-07-09 1998-06-24 90; Conservative Similarity FILING DATE: FILING DATE: RESULT 14 US-09-989-293A-377 Query Match Best Local S Matches 90 PRIOR
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CURRENT APPLICATION NUMBER: 05/049787

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PRIOR FILING DATE: 1997-06-16

PRIOR PELING DATE: 1997-06-16

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-17

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PRIOR APPLICATION NUMBER: 60/065186

PRIOR PELING DATE: 1997-11-13

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TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Ferrara, Napoleone
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                                    APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Tumas, Daniel
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         GENERAL INFORMATION:
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Transmembrane Polypeptides and Nucleic
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TITLLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C61
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CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watnabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
                                                                                                                                                                                        Gerritsen, Mary E.
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                                       Desnoyers, Luc
Eaton, Dan L.
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100.0%; Score 462; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088217
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